

	Mouse lysophospholipase
	Human hydrolyase-11
	Drosophila melanogaster
	Human prostate carcinoma
	Novel human diaphanous
	Drosophila melanogaster
	Mitesterase which hydrolyzes
	Microbial esterases
	Human lysophospholipase
	Plant SDF encoded protein
	Hedidically active
	Zea mays protein f
	Human secreted protein
	Human secreted protein
	Human secreted protein
	Human lysophospholipase
	Secreted protein #
	Human secreted protein
	Hedidically active
	Human MDR7 SEQ ID
	Plant SDF encoded protein
	Plant SDF encoded protein
	Chlamydia pneumoniae
	Human 5' ESR sequence
	Listeria monocytogenes
	Araldisopsis thalassia
	Streptococcus polydysenteriae
	Drosophila melanogaster
	Human protein sequence
	Group B streptococcus
	Mycobacterium tuberculosis
	Amino acid sequence
	Protein involved in

PR	12-FEB-1998:	98US-0022940.
PR	29-APR-1997:	97US-0844120.
XX	(INCY-)	INCYTE PHARM INC.
XX	Hillman JL,	Murry LE, Shah P;
XX	WPI: 1999-326512/27.	
DR	N-PSSD:	AAX56266.
PP	New human lysophospholipase (NHLP)	polypeptides and polynucleotides
PP	which identify and encode NHLP	
PS	Claim 1; Fig 1; 66pp; English.	
XX	The present sequence is human lysophospholipase (NHLP). The present	
CC	Invention also describes a method for treating or preventing a disorder	
CC	of cell proliferation (e.g. arteriosclerosis, atherosclerosis, bursitis,	
CC	cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,	
CC	prioxymal nocturnal haemoglobinuria, polygythaemia vera, psoriasis,	
CC	primary thrombocytopenia, and cancers), inflammation (e.g. Addison's	
CC	disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a	
CC	disorder of the immune response (e.g. AIDS, allergies, ankylosing	
CC	spondylitis, autoimmune haemolytic anaemia) by administering an	
CC	antagonist to NHLP. NHLP proteins, antagonists, antibodies, agonists,	
CC	complementary sequences or vectors may be administered in combination	
CC	with other therapeutic agents. Antibodies which specifically bind to	
CC	NHLP may be used for the diagnosis of disorders characterized by	
CC	expression of NHLP or in assays to monitor patients being treated with	
CC	NHLP or agonists. The polynucleotides (PNS) encoding NHLP or fragments	
CC	may be used therapeutically. In one aspect, the complement of the	
CC	polynucleotides may be used where it would be desirable to block the	
CC	transcription of the mRNA. Complementary molecules may be used to	
CC	modulate NHLP activity or to achieve regulation of gene activity.	
CC	Diagnostically, the PNS may be used to detect and quantitate gene	
CC	expression in biopsied tissues in which expression of NHLP may be	
CC	correlated with disease.	
XX		
SQ	Sequence 207 AA:	
	Query Match 98.6%; Score 1055; DB 20; Length 207;	
	Best Local Similarity 99.5%; Pred. No. 6.2e-113;	
	Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 MCGNNMSTPLPAIVPARAKATAAATVFLGIGDTGPYPRTPLMNANNAAMPSPDIIIGISPD 60	
DB	1 MCGNNMSTPLPAIVPARAKATAAATVFLHGLGDTGPVPRTPLMNANNAAMPSPFIIGISPS 60	
OY	61 QEDSGSIRKAENIKRALIDQEVKNGIPSNRIILGGFSGGALSIVTALTTOOKLAGVTAL 120	
DB	61 QEDSGSIRKAENIKRALIDQEVKNGIPSNRIILGGFSGGALSIVTALTTOOKLAGVTAL 120	
OY	121 SFLLPLRXSFPOGPIGGANDISILIOCHGDCEPLVLFMGSLTVEKLTLVNPNANTFT 180	
DB	121 SFLLPLRXSFPOPIGARGDISIILIOCHGDCEPLVLFMGSLTVEKLTLVNPNANTFT 180	
OY	181 YEGMMHSSCOQEMMDVKOFIDKILLPI 207	
DB	181 YEGMMHSSCOQEMMDVKOFIDKILLPI 207	
RESULT 2		
ID	AAG75019 standard; Protein; 219 AA.	
XX	AAG75019;	
AC		
XX	03-SEP-2001 (first entry)	
DT		
XX	Human colon cancer antigen protein SEQ ID NO:5783.	
DE		
XX	Human: colon cancer; colon cancer antigen; diagnosis; detection;	
KW	colorectal carcinoma.	

XX	Homo sapiens.
OS	
PX	MO200122920-A2.
NN	
PD	05-APR-2001.
XX	
PF	28-SEP-2000; 2000WO-US26524.
PR	29-SEP-1999; 99US-0157137.
PR	03-NOV-1999; 99US-0163280.
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Barash SC, Birse CE, Rosen CA;
DR	WPI: 2001-235357/24.
DR	N-PSDB; AAH34424.
XX	
PT	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX	useful for preventing, diagnosing and/or treating colorectal cancers -
XX	Claim 11; Page 7301-7302; 9803pp; English.
PS	
XX	AAB32943 to AAB37195 and AAG73514 to AAG77788 represent human colon
CC	cancer-associated nucleic acid molecules (N) and proteins (P), where
CC	the proteins are collectively known as colon cancer antigens. The colon
CC	cancer antigens have cytostatic activity and can be used in gene
CC	therapy and vaccine production. N and P may be used in the prevention,
CC	diagnosis and treatment of diseases associated with inappropriate P
CC	expression. For example, N and P may be used to treat disorders
CC	associated with decreased expression by rectifying mutations or deletions
CC	in a patient's genome that affect the activity of P by expressing
CC	inactive proteins or to supplement the patients own production of P.
CC	Additionally, N may be used to produce the colon cancer-associated Ps,
CC	by inserting the nucleic acids into a host cell and culturing the cell
CC	to express the proteins. N and P can be used in the prevention, diagnosis
CC	and treatment of colorectal carcinomas and cancers. AAB37196 to AAB37204
CC	and AAB77789 represent sequences used in the exemplification of the
CC	present invention.
CC	N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC	missing at time of publication, meaning no sequences are present for
CC	SEQ ID NO:1027 to 1052, 7921 and 7922.
XX	
SQ	Sequence 219 AA:
Query Match	96.9%; Score 1037; DB 22; Length 219;
Best Local Similarity	97.6%; Pred. No. Be-111;
Matches 203; Conservative	0; Mismatches 5; Indels 0; Gaps 0
QY	1 MCGNNNSTPLPALVPARAKATAAIVFLHGIGDGTGPRPYTLNANNVAMPMSFIDIGSPDS 60
DB	12 MCGNNSTPLPALVPARAKATAAIVFLHGIGDGTGPRPYTLNANNVAMPMSFIDIGSPDS 71
QY	61 QEDESGIKOAENIKALIDQEVKNGLIPSNRIILGGSSOGALSLYTALTTOOKLAAVTAL 120
DB	72 QEDESGIKOAENIKALIDQEVKNGLIPSNRIILGGSSOGALSLYTALTTOOKLAAVTAL 131
QY	121 SFLLPLRXSPPQPGIGANDDISIIOCHGCDPLVLPMFGSLIVERLKTLVNPANTYFTK 180
DB	132 SCWLPLRASFPQPGIGANDDISIIOCHGCDPLVLPMFGSLIVERLKTLVNPANTYFTK 191
QY	181 YEGMMHSSCOEQEMADVKQFITDKLLPID 208
DB	192 YEGMMHSSCOEQEMADVKQFITDKLLPID 219
RESULT 3	
AAAY09531	
ID	AAAY09531 standard; Protein; 230 AA.
AC	AAAY09531;
XX	

DT 19-JUL-1999 (first entry)
 XX
 DE Human lysophospholipase extended NHLP.
 XX
 KW Human; lysophospholipase; NHLP; cell proliferation; arteriosclerosis;
 KW atherosclerosis; bursitis; cirrhosis; hepatitis; myelofibrosis;
 KW mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
 KW polycythaemia vera; psoriasis; primary thrombocytopenia; cancer;
 KW inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;
 KW immune response; ankylosing spondylitis; autoimmune haemolytic anaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO9849319-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US08782.
 XX
 PR 12-FEB-1998; 98US-0022940.
 XX
 PR 29-APR-1997; 97US-0844120.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Murry LE, Shah P;
 XX
 DR WPI: 1999-326512/27.
 DR N-PSDB; AAX56267.
 XX
 PT New human lysophospholipase (NHLP) polypeptides and polynucleotides
 XX which identify and encode NHLP
 XX
 PS Claim 1; Fig 2; 66pp; English.
 XX
 CC The present sequence is human lysophospholipase (NHLP). The present
 CC invention also describes a method for treating or preventing a disorder
 CC of cell proliferation (e.g. arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,
 CC paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis,
 CC primary thrombocytopenia, and cancers); inflammation (e.g. Addison's
 CC disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a
 CC disorder of the immune response (e.g. AIDS, allergies, ankylosing
 CC spondylitis, autoimmune haemolytic anaemia) by administering an
 CC antagonist to NHLP. NHLP proteins, antagonists, antibodies, agonists,
 CC complementary sequences or vectors may be administered in combination
 CC with other therapeutic agents. Antibodies which specifically bind to
 CC NHLP may be used for the diagnosis of disorders characterized by
 CC expression of NHLP or in assays to monitor patients being treated with
 CC NHLP or agonists. The polynucleotides (PNS) encoding NHLP or fragments
 CC may be used therapeutically. In one aspect, the complement of the
 CC polynucleotides may be used where it would be desirable to block the
 CC transcription of the mRNA. Complementary molecules may be used to
 CC modulate NHLP activity or to achieve regulation of gene activity.
 CC Diagnostically, the PNS may be used to detect and quantitate gene
 CC expression in biopsied tissues in which expression of NHLP may be
 CC correlated with disease.
 CC
 XX
 SQ Sequence 230 AA;
 Query Match 96.6%; Score 1034; DB 20; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.9e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;
 Oy 1 MCGNNMSTPLPAIVPAARKATAAVIFLHIGDGTG-----PVRP 38
 Db 1 MCGNNMSTPLPAIVPAARKATAAVIFLHIGDGTGMAEAFAGIRSSHIIKYICPHAVRP 60
 Oy 39 VTLMNNVAMPSPWFDITIGLSPDSOEDSGIKQAENIKALIDQEVKNGIPSNRIILGGSQ 98
 Db 61 VTLMNNVAMPSPWFDITIGLSPDSOEDSGIKQAENIKALIDQEVKNGIPSNRIILGGSQ 120
 Oy 99 GGALSLVTALTTOOKLAGVTAFLPLRXSFPOGPIGAGNRDISIIQCHGDCDPLVPLM 158
 ||||||||||||||||||||| ||| |||||||||||||||||||||||||||||

Db 121 GGALSLVTALTTOOKLAGVTAFLSCWPLRASFPOGPIGAGNRDISIIQCHGDCDPLVPLM 180
 Oy 159 FGSILVEKTLVNPANVTFTYEGAMHSSCOQEMADYKQFIDKLEPPID 208
 Db 181 FGSILVEKTLVNPANVTFTYEGAMHSSCOQEMADYKQFIDKLEPPID 230
 RESULT 4
 ID AA085132 standard; Protein; 230 AA.
 XX
 AC AA085132;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human lysophospholipase I #1.
 XX
 KW Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antihypertensive; cardiac; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200210185-A1.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-US22975.
 XX
 PR 31-JUL-2000; 2000US-0629645.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Wyatt JR;
 XX
 DR WPI: 2002-188720/24.
 DR N-PSDB; ABR37030.
 XX
 PT Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX
 PS Disclosure; Page 88-89; 131pp; English.
 XX
 CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridizes with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. AA085132-AA085136
 CC represent lysophospholipase I amino acid sequences of the invention.
 CC
 XX
 SQ Sequence 230 AA;
 Query Match 96.6%; Score 1034; DB 23; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.9e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;
 Oy 1 MCGNNMSTPLPAIVPAARKATAAVIFLHIGDGTG-----PVRP 38
 Db 1 MCGNNMSTPLPAIVPAARKATAAVIFLHIGDGTGMAEAFAGIRSSHIIKYICPHAVRP 60
 Oy 39 VTLMNNVAMPSPWFDITIGLSPDSOEDSGIKQAENIKALIDQEVKNGIPSNRIILGGSQ 98
 Db 61 VTLMNNVAMPSPWFDITIGLSPDSOEDSGIKQAENIKALIDQEVKNGIPSNRIILGGSQ 120
 Oy 99 GGALSLVTALTTOOKLAGVTAFLPLRXSFPOGPIGAGNRDISIIQCHGDCDPLVPLM 158
 ||||||||||||||||||||| ||| |||||||||||||||||||||||||||||

Db 121 GGAISLTALTTOOKLAGVTALSCWLPRLASFPOGPFGANRDISIIQCHGDCDPLVPLM 180

Qy 159 FGSILVEKIKTLVNPANVTEFKTYEGMMHSSCOQEMMDVKQFIDKLLPDPID 208
 |||||
 Db 181 FGSILVEKIKTLVNPANVTEFKTYEGMMHSSCOQEMMDVKQFIDKLLPDPID 230

RESULT 5
 AA085134
 ID AA085134 standard; Protein; 230 AA.
 XX
 AC AA085134;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human lysophospholipase I #2.
 XX
 KW Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antilipemic; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antitense gene therapy.
 KW
 OS Homo sapiens.
 XX
 PN WO200210185-A1.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-US22975.
 XX
 PR 31-JUL-2000; 2000US-0629645.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Wyatt JR.
 DR WPI: 2002-188720/24.
 DR N-PSDB: ABR37045.
 XX
 PT Novel antitense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX
 PS Disclosure; Page 94-95; 131pp; English.
 XX
 CC The invention relates to an antitense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antitense gene therapy. AA085132-AA085136
 CC represent lysophospholipase I amino acid sequences of the invention.
 XX
 SQ Sequence 230 AA:

Query Match 96.6%; Score 1034; DB 23; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.9e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

Qy 1 MCGNNMSTPLPAIVPARKKATAAIVFLHGLGDTG-----PVRP 38
 |||||
 Db 1 MCGNNMSTPLPAIVPARKKATAAIVFLHGLGDTGHHGMAEPAFACIRSSHITKTCPPHAPVRP 60
 |||||

Qy 39 VTLNMNVAMPSPWDIIIGLSPDSQEDSGIKQAANIKALIDQEVKNIGPSNRITILGFSQ 98
 |||||
 Db 61 VTLNMNVAMPSPWDIIIGLSPDSQEDSGIKQAANIKALIDQEVKNIGPSNRITILGFSQ 120
 |||||

Qy 99 GGAISLTALTTOOKLAGVTALSCWLPRLASFPOGPFGANRDISIIQCHGDCDPLVPLM 158
 |||||

Db 121 GGAISLTALTTOOKLAGVTALSCWLPRLASFPOGPFGANRDISIIQCHGDCDPLVPLM 180

Qy 159 FGSILVEKIKTLVNPANVTEFKTYEGMMHSSCOQEMMDVKQFIDKLLPDPID 208
 |||||
 Db 181 FGSILVEKIKTLVNPANVTEFKTYEGMMHSSCOQEMMDVKQFIDKLLPDPID 230

RESULT 6
 AAB53451
 ID AAB53451 standard; Protein; 263 AA.
 XX
 AC AAB53451;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human colon cancer antigen protein sequence SRQ ID NO:991.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antineutrophic; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 KW
 OS Homo sapiens.
 XX
 PN WO200055351-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05883.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 DR WPI: 2000-587534/55.
 DR N-PSDB: AAC98208.
 XX
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 XX
 PS Claim 11; Page 1568-1569; 2104pp; English.
 XX
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnary, nephrotropic, antineutrophic and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC treatment and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 263 AA:

Query Match 96.6%; Score 1034; DB 21; Length 263;
 Best Local Similarity 89.1%; Pred. No. 2.3e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

Qy 1 MCGNNMSTPLPAIVPARKKATAAIVFLHGLGDTG-----PVRP 38
 |||||

Db 34 MCGNNSTPLPAIVPAARKATAAVIFLHGLDGTGHGMAEAFAGIRSSHIIKICPHAPVR 93
 QY 39 VTLMNNVAMPSPFDDIIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 94 VTLMNNVAMPSPFDDIIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 153
 QY 99 GGALSLTYALTTOOKLAGVTALSFLLPLRXSPGPGPIGAGNRDISIIQCHGDCDPLVPLM 158
 Db 154 GGALSLTYALTTOOKLAGVTALSCWLPTRASFPQGPPIGAGNRDISIIQCHGDCDPLVPLM 213
 QY 159 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 208
 Db 214 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 263
 RESULT 7
 ABG07277
 ID ABG07277 standard; Protein: 275 AA.
 AC ABG07277;
 XX 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #7268.
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN MO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-0508631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEO INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI: 2001-639362/73.
 DR N-PSDB: AAS71464.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20; SEQ ID No 37636; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 275 AA;
 Query Match 96.6%; Score 1034; DB 22; Length 275;
 Best Local Similarity 89.1%; Pred. No. 2.5e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;
 QY 1 MCGNNSTPLPAIVPAARKATAAVIFLHGLDGTGHGMAEAFAGIRSSHIIKICPHAPVR 38
 Db 46 MCGNNSTPLPAIVPAARKATAAVIFLHGLDGTGHGMAEAFAGIRSSHIIKICPHAPVR 105
 QY 39 VTLMNNVAMPSPFDDIIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 106 VTLMNNVAMPSPFDDIIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 165
 QY 99 GGALSLTYALTTOOKLAGVTALSFLLPLRXSPGPGPIGAGNRDISIIQCHGDCDPLVPLM 158
 Db 166 GGALSLTYALTTOOKLAGVTALSCWLPTRASFPQGPPIGAGNRDISIIQCHGDCDPLVPLM 225
 QY 159 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 208
 Db 226 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 275
 RESULT 8
 AAB82669
 ID AAB82669 standard; Protein: 230 AA.
 AC AAB82669;
 XX 02-OCT-2001 (first entry)
 DE Human brain lysophospholipase.
 KW Lysophospholipase; human; brain; lysophospholipid; atherosclerosis;
 KW hypellipidemia; dysrhythmia; myocardial ischaemia; demyelination;
 KW vasotropic; antiatherosclerotic; antilipemic; neuroprotective;
 KW therapy; lysopla.
 OS Homo sapiens.
 PN MO200155166-A1.
 PD 02-AUG-2001.
 PF 28-JAN-2000; 2000WO-0502319.
 PR 28-JAN-2000; 2000US-0493601.
 XX (REGC) UNIV CALIFORNIA.
 PA Dennis EA, Wang A;
 PI WPI: 2001-483215/52.
 DR N-PSDB: AAB26336.
 XX Novel recombinant lysophospholipid-specific human brain
 PT lysophospholipase enzyme useful for treating disease states having
 PT elevated concentrations of lysophospholipids, such as atherosclerosis,
 PT hyperlipidaemia -
 PS Claim 4; Fig 1; 38pp; English.
 XX The present sequence is that of human brain lysophospholipid-specific
 CC lysophospholipase (lysopla), a novel member of the K/L hydrolase
 CC family having a catalytic site composed of Ser-119, Asp-174 and
 CC His-208. Lysoplas are critical enzymes that act on biological

CC membranes to regulate the multifunctional lysophospholipids;
 CC increased levels of lysophospholipids are associated with a host of
 CC diseases. The enzyme is widely distributed in almost all tissues,
 CC although levels vary. Lysopla cDNA (see AAH26336) was obtained by
 CC PCR amplification of human brain cDNA using primers (see AAH26337-38)
 CC based on human sequences identified by database screening using a
 CC mouse sequence. The PCR product was expressed in *Escherichia coli*
 CC BL21 (DE3) cells using vector pET28a(a). The recombinant lysopla
 CC protein, which included an N-terminal 6His tag and thrombin cleavage
 CC site, was recovered on an Ni-NTA column. Kinetic analysis showed
 CC that human lysopla displays apparent co-operativity and surface
 CC dilution kinetics. The recombinant lysopla can be used in the
 CC treatment of disease states having elevated concentrations of
 CC lysophospholipids, such as atherosclerosis, hyperlipidaemia, lethal
 CC dysrhythmia in myocardial ischaemia and segmental demyelination of
 CC peripheral nerves. The lysopla may be supplied to the
 CC enzyme-deficient patient by infusion or by gene therapy (both
 CC claimed). Also claimed is a method of inhibiting human brain
 CC lysopla activity using methyl arachidonyl fluorophosphates.

SO Sequence 230 AA;

Query Match 96.1%; Score 1028; DB 22; Length 230;
 Best Local Similarity 88.7%; Pred. No. 9,4e-110;
 Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;

OY 1 MCGNNMSTPLPAVPAARKATAVIFLHGLGDTG-----PVRP 38
 DB 1 MCGNNMSTPLPAVPAARKATAVIFLHGLGDTGHWMAEFAFGINSHTKTCYCPHAPVRP 60
 OY 39 VTLNNVAMPSPWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNKIPSNRIILGGFSQ 98
 DB 61 VTLNNVAMPSPWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNKIPSNRIILGGFSQ 120
 OY 99 GGLSLYTAITTOOKLAGVTALSFLLPLRXSFPGCGPIGANDRISILQCHGDCDPLVPLM 158
 DB 121 GGLSLYTAITTOOKLAGVTALSCWLPRLASFSQGPINSANRDISVLCQCHGDCDPLVPLM 180
 OY 159 FGSILVEKLTLYNPANVTFTYEGMMHSSCOQEMDMVKQFIDKLPPID 208
 DB 181 FGSILVEKLTLYNPANVTFTYEGMMHSSCOQEMDMVKQFIDKLPPID 230

RESULT 9
 AAU85133
 ID AAU85133 standard; Protein; 230 AA.

XX AC AAU85133;
 XX DT 08-MAY-2002 (first entry)
 XX DE Mouse lysophospholipase I #1.
 XX KW Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antilipemic; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy.
 XX OS Mus musculus.
 XX PN WO200210185-A1.
 XX PD 07-FEB-2002.
 XX PF 20-JUL-2001; 2001WO-US22975.
 XX PR 31-JUL-2000; 2000US-0629645.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Bennett CF, Wyatt JR;
 XX DR WPI; 2002-188720/24.

DR N-PSDB; ABK37037.
 XX Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX Disclosure; Page 92-93; 131pp; English.

CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
 CC represent lysophospholipase I amino acid sequences of the invention.

SO Sequence 230 AA;

Query Match 90.5%; Score 968; DB 23; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.6e-103;
 Matches 188; Conservative 8; Mismatches 12; Indels 22; Gaps 1;

OY 1 MCGNNMSTPLPAVPAARKATAVIFLHGLGDTG-----PVRP 38
 DB 1 MCGNNMSPMPVAVPAARKATAVIFLHGLGDTGHWMAEFAFGINSHTKTCYCPHAPVRP 60
 OY 39 VTLNNVAMPSPWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNKIPSNRIILGGFSQ 98
 DB 61 VTLNNVAMPSPWFDIIGLSPDSQEDSGIKQAETVALIDQEVKNKIPSNRIILGGFSQ 120
 OY 99 GGLSLYTAITTOOKLAGVTALSFLLPLRXSFPGCGPIGANDRISILQCHGDCDPLVPLM 158
 DB 121 GGLSLYTAITTOOKLAGVTALSCWLPRLASFSQGPINSANRDISVLCQCHGDCDPLVPLM 180
 OY 159 FGSILVEKLTLYNPANVTFTYEGMMHSSCOQEMDMVKQFIDKLPPID 208
 DB 181 FGSILVEKLTLYNPANVTFTYEGMMHSSCOQEMDMVKQFIDKLPPID 230

RESULT 10
 AAY69296
 ID AAY69296 standard; Protein; 214 AA.

XX AC AAY69296;
 XX DT 19-JUN-2000 (first entry)
 XX DE A human lysophospholipase protein designated CBFLH05.
 XX KW Human; lysophospholipase; CBFLH05; liver disease; cancer;
 KW autoimmune disease; kidney disorder; vaccine.
 XX OS Homo sapiens.
 XX PN WO200009556-A1.
 XX PD 24-FEB-2000.
 XX PF 11-AUG-1998; 98WO-CN00164.
 XX PR 11-AUG-1998; 98WO-CN00164.
 XX PA (UTSH-) UNIV SHANGHAI SECOND MEDICAL.
 XX PI Zhou J, Mao M, Ye M, Zhang Q;
 XX DR WPI; 2000-224281/19.
 XX DR N-PSDB; AAZ61501.

PT New human lysophospholipase gene (designated CBFLH05) polypeptides and
 PT polynucleotides used to identify agonists, antagonists and inhibitors
 PT for use in (gene) therapy -

PS Claim 2, Page 23; 36pp; English.

CC The present sequence represents a human lysophospholipase protein
 CC (designated CBFLH05). CBFLH05 polypeptides may be used for
 CC identifying agonists and antagonists/inhibitors, and for detecting
 CC and treating diseases associated with inappropriate CBFLH05 activity
 CC or levels. CBFLH05 polypeptides and polynucleotides, agonists,
 CC antagonists and antibodies are used for the treatment of liver diseases,
 CC cancer, autoimmune diseases, and kidney disorders. The polynucleotide
 CC is also useful as a source of primers and probes, and also for detecting
 CC the above diseases. The polypeptide may also be used as a vaccine.

XX Sequence 214 AA:

Query Match 88.7%; Score 949; DB 21; Length 214;

Best Local Similarity 88.4%; Pred. No. 1,le-100;

Matches 191; Conservative 4; Mismatches 11; Indels 10; Gaps 2;

QY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVPRVTLMNNVAMPSPWD 52
 DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTGHWAEAFAGIR--SSHIKYICPHAFD 58
 QY 53 IIGLSPDSQEDSGIKQAENIKALIDQVKNIGIPSNRIILGGFSOGALSLYALTTQQ 112
 DB 59 IIGLSPDSQEDSGIKQAENIKALIDQVKNIGIPSNRIILGGFSOGALSLYALTTQQ 118
 QY 113 KLAGYALSLFLPLRXSPGPGIGANRDISILQCHGDCDPLVPLMFSLTVEKLKTLYN 172
 DB 119 KLAGYALSLFLPLRXSPGPGIGANRDISILQCHGDCDPLVPLMFSLTVEKLKTLYN 178
 QY 173 PANVTFTKEGMMHSSCOQEMMDVKQFTDKLLPID 208
 DB 179 PANVTFTKEGMMHSSCOQEMMDVKQFTDKLLPID 214

RESULT 11

AAU85136
 ID AAU85136 standard; Protein; 230 AA.

AC AAU85136;

DT 08-MAY-2002 (first entry)

DE Mouse lysophospholipase I #3.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antiinflammatory; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy.

OS Mus musculus.

PN WO200210185-A1.

PD 07-FEB-2002.

XX 20-JUL-2001; 2001WO-US22975.

PR 31-JUL-2000; 2000US-0629645.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Wyatt JR;

DR WPI; 2001-188720/24.

DR N-PSDB; ABK37048.

PT Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis

PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX
 PS Disclosure; Page 98-99; 131pp; English.

CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
 CC represent lysophospholipase I amino acid sequences of the invention.

XX Sequence 230 AA:

Query Match 88.5%; Score 947; DB 23; Length 230;

Best Local Similarity 80.4%; Pred. No. 2e-100;

Matches 185; Conservative 8; Mismatches 15; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVPR 38
 DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTGHWAEAFAGIKSPHIKYPHAPVP 60
 QY 39 VTLNNVAMPSPWDITGLSPDSQEDSGIKQAENIKALIDQVKNIGIPSNRIILGGFSQ 98
 DB 61 VTLNNVAMPSPWDITGLSPDSQEDSGIKQAENIKALIDQVKNIGIPSNRIILGGFSQ 120
 QY 99 GGALSLTALTTOOKLAGVATLSFLPLRXSPGPGIGANRDISILQCHGDCDPLVPLM 158
 DB 121 GGALSLTALTTOOKLAGVATLSFLPLRXSPGPGINSNRRISVLQCHGDCDPLVPLM 180
 QY 159 FGSILTVEKLTLVNPANVTFTKEGMMHSSCOQEMMDVKQFTDKLLPID 208
 DB 181 FGSILTVEKLTLVNPANVTFTKEGMMHSSCOQEMMDVKQFTDKLLPID 230

RESULT 12

AAU82796
 ID AAU82796 standard; Protein; 231 AA.

AC AAU82796;

DT 13-FEB-2001 (first entry)

DE Human hydrolase-like molecule 7 protein.

XX Hydrolase-like molecule; human; cell proliferation disorder;
 KW autoimmune; cancer; AIDS; acquired immune deficiency syndrome.

OS Homo sapiens.

PN US6132964-A.

PD 17-OCT-2000.

XX 06-FEB-1998; 98US-0013881.

PR 06-FEB-1998; 98US-0013881.

PA (INCY-) INCYTE PHARM INC.

PI Bandman O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;

DR WPI; 2001-006133/01.

DR N-PSDB; AAC60229.

PT New human hydrolase-like molecules (HILMs) and polynucleotides encoding
 PT the HILMs, useful for diagnosing, treating or preventing cell
 PT proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
 PT asthma) -

XX Claim 1; Column 53-54; 38pp; English.
 PS
 CC The present invention relates to isolated and purified cDNA encoding a
 CC human hydrolase-like molecule (HLM), designated HLM-1 to HLM-8. The
 CC HLM DNAs and polypeptides are useful for diagnosing, treating or
 CC preventing cell proliferation disorders and autoimmune disorders. Cell
 CC proliferation disorders include cancers, autoimmune disorders include
 CC AIDS (acquired immune deficiency syndrome). The present sequence
 CC is a HLM protein of the invention.
 XX
 SQ Sequence 231 AA;
 Query Match 66.6%; Score 713; DB 22; Length 231;
 Best Local Similarity 60.8%; Pred. No. 1.8e-73;
 Matches 141; Conservative 28; Mismatches 37; Indels 26; Gaps 3;
 OY 1 MCGNNSTPL---PAIVPAARKATAVIFLHGLDGTG-----P 35
 DB 1 MCGNTSVPLTLDAATVSGAERETAIVFLHGLDGTGSMADALSTRILPHVKYICPNAP 60
 OY 36 VRPVTLNMMVAMPSEWDIIGLSPDSESGIKQAENIKALIDQEVKNGIPSRITLIG 95
 DB 61 RIVPTLNMKVMPSWFDLMLSPDAPEDEAGIKKAENIKALIEHMKNGITANRIVLGG 120
 OY 96 FSGGALSLTYTALTTOOKLAGVTALSFLLPLRXSPQGPFGANRDISILQCHGDCDPLV 155
 DB 121 FSGGALSLTYTALTCTCHPLAGIALSCWPLRHAFPOANGSA-KDLATLQCHGELDPV 179
 OY 156 PLMFGLSVLEKLTLPANAVTEFKYEGMMHSSCOQEMDKVOPIDKLLPPI 207
 DB 180 PVRFGLTAELKLRVTPAVQCFKTYPGVHSSCOPEMAVKEFLKLLPV 231

RESULT 13
 ABB67341
 ID ABB67341 standard; Protein; 216 AA.
 XX
 AC ABB67341;
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 28815.
 XX
 KW Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR N-PSDB; ABL11444.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 28815; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72027).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 216 AA;
 Query Match 45.8%; Score 490; DB 22; Length 216;
 Best Local Similarity 48.1%; Pred. No. 7.9e-48;
 Matches 103; Conservative 24; Mismatches 61; Indels 26; Gaps 3;
 OY 11 PAIVPAARKATAVIFLHGLDGTG-----PVRPVTLNMMVAMP 48
 DB 4 PVIYEAIVKQRTILIFMGLDGTGHGSSALAIRPFPMKVICPTAPTOPVSLNAGFRMP 63
 OY 49 SWFDIIGLSPDSESGIKQAENIKALIDQEVKNGIPSRITLIGFSGGALSLTYAL 108
 DB 64 SWFDLKTLDIGAPDEDEPGIGARDSVHGMIOKEISAGIPANRIVLIGFSGGALATYSAL 123
 OY 109 TTOOKLAGVTALSFLLPLRXSPQGPFGANRDISILQCHGDCDPLVPLMFGLSVLEK 168
 DB 124 TYDQPLAGVVALSCWPLHKOFPQAKV--SDVPIRQAHGDXDPVVPYKFGOLSASL 181
 OY 169 TLVNPAVTEFKYEGMMHSSCOQEMDKVOPIDK 202
 DB 182 SPMK--NTYFKTYSGLSHSSSDDEMDVDKDIISK 213

RESULT 14
 AAY48392
 ID AAY48392 standard; Protein; 119 AA.
 XX
 AC AAY48392;
 DT 08-DEC-1999 (first entry)
 XX
 DE Human prostate cancer-associated protein 89.
 XX
 KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
 KW cancer; tissue specificity; human.
 XX
 OS Homo sapiens.
 XX
 PN DE19811194-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 10-MAR-1998; 98DE-1011194.
 XX
 PR 10-MAR-1998; 98DE-1011194.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX
 DR WPI: 1999-519629/44.
 DR N-PSDB; AA23516.
 XX
 PT New nucleic acid expressed at high level in normal prostatic tissue and
 PT encoded polypeptides, used to treat cancer and screen for therapeutic
 PT agents -
 XX
 PS Claim 22; 158; 194pp; German.
 CC This invention describes novel nucleic acid sequences (A) that are
 CC expressed at high level in normal prostatic tissue. Polypeptides (I)
 CC encoded by (A) are used: (a) for identifying agents for treatment of
 CC prostatic cancer and (b) for therapy of prostate cancer, optionally

CC where expressed by gene therapy methods. (A) is also used to isolate
 CC full-length genes (for gene therapy) and for recombinant production of
 CC (I), which can be used to raise specific antibodies. (A) are identified
 CC by assembly of ESTs (expressed sequence tags) before these are analyzed
 CC for expression pattern (tissue specificity). This approach eliminates
 CC many of the false results, as regards tissue specificity, associated
 CC with known methods that use single (usually short) ESTs. AA48304-Y48456
 CC represent peptides encoded by the expressed sequence tags described in
 CC the method of the invention.

XX Sequence 119 AA;

Query Match 38.0%; Score 406.5; DB 20; Length 119;
 Best Local Similarity 64.2%; Pred. No. 1.3e-38;

Matches 77; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

OY 88 SNRIILGFSGGALSLYALTTOOKLAGYALSLPLLRKSPFGPIGANDISILQC 147
 Db 1 ANRIYLGFSGGALSLYALTTCPHLAGIYALSCWLP LHRAPFOANGSA-KDLAILQC 59

OY 148 HGDDPLVPLMEGSLVEKTKTIVNPVPEKTEGMMHSSCOEEMDVQOFIDKLPI 207
 Db 60 HGEIDPMVPVFGALTAELKLSVTPARVOPKTPGVHSSCPQEMAAYEFLEKLIPV 119

RESULT 15

ABG07276 standard; Protein; 89 AA.

XX ABG07276;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #7267.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS71463.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 20; SEQ ID NO 37635; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 89 AA;

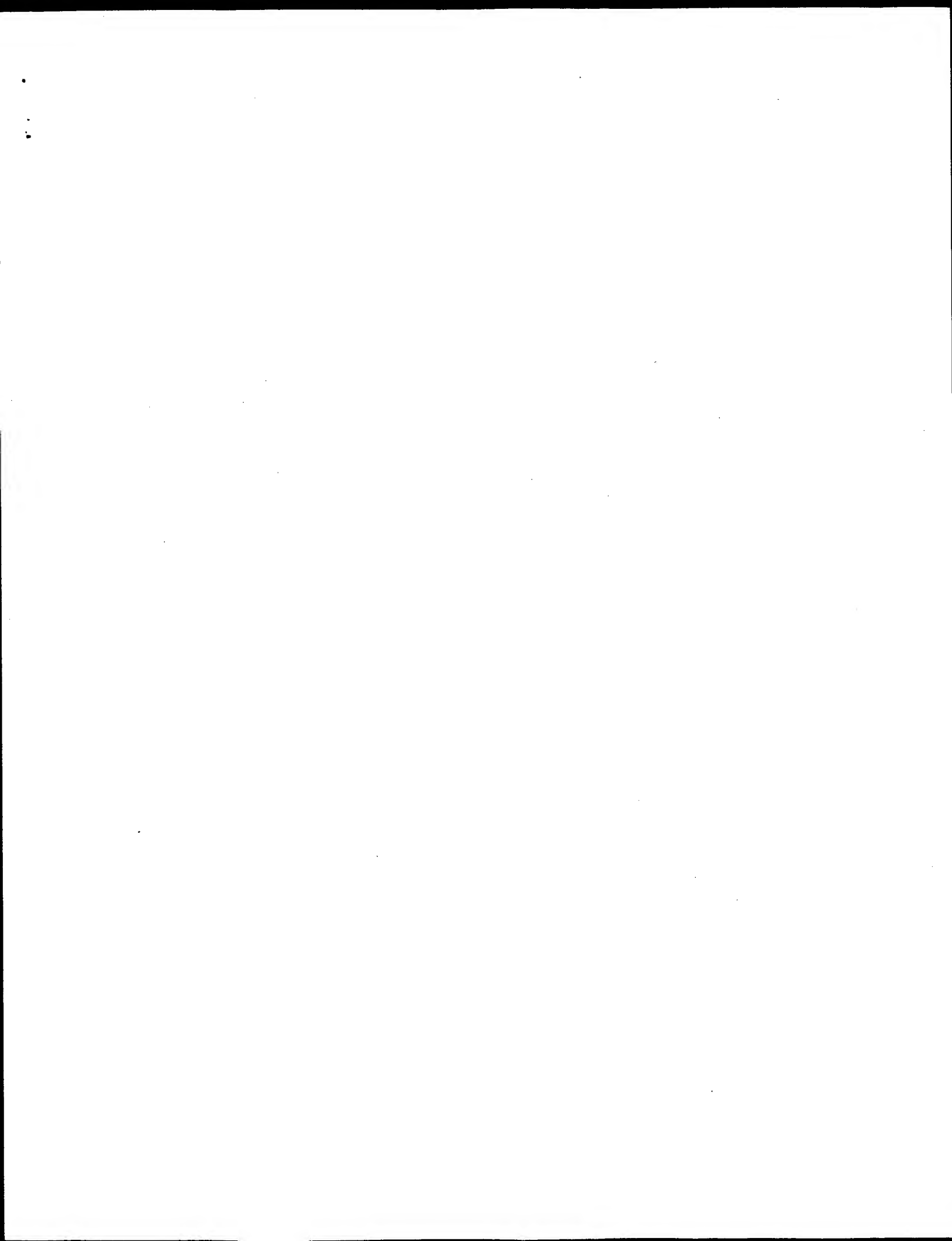
Query Match 33.3%; Score 356; DB 22; Length 89;
 Best Local Similarity 73.3%; Pred. No. 5.7e-33;

Matches 77; Conservative 2; Mismatches 10; Indels 16; Gaps 2;

OY 6 MSTPLPAIVPARKATAAVIFLGLDGTGPVPTLNMNVAMPSPFDIIGLSPDSQEDS 65
 Db 1 MSAPLPAIVPATKATNAVIFLGLDGTG-----HRWIEAFA--DSQEDP 44

OY 66 GIKQAAMNIKALIDQEVKNGIPSNRIILGFSGGALSLYALT 110
 Db 45 GIKQAAMNIKALIDQEVKNGIPSNRIILGFSGGALSLYALT 89

Search completed: January 19, 2003, 03:19:39
 Job time : 142 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 19, 2003, 03:17:20 ; Search time 37 Seconds
(Without alignments)
165.405 Million cell updates/sec

Title: US-09-988-982-1
Perfect score: 1070
Sequence: 1 MCGNNSTPLPAIVPARKA.....COEEMDVKQFIDKLLEPID 208

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
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- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1068	99.8	208	US-08-844-120-1	Sequence 1, Appl1
2	1068	99.8	208	US-09-213-394-1	Sequence 1, Appl1
3	1055	98.6	207	US-09-022-940-1	Sequence 1, Appl1
4	1055	98.6	207	US-09-216-386-1	Sequence 1, Appl1
5	1034	96.6	230	US-09-022-940-3	Sequence 3, Appl1
6	1034	96.6	230	US-09-216-386-3	Sequence 3, Appl1
7	958	89.5	230	US-08-844-120-3	Sequence 3, Appl1
8	958	89.5	230	US-09-022-940-5	Sequence 5, Appl1
9	958	89.5	230	US-09-216-001-3	Sequence 3, Appl1
10	958	89.5	230	US-09-216-386-5	Sequence 5, Appl1
11	958	89.5	230	US-08-878-862-3	Sequence 3, Appl1
12	958	89.5	230	US-09-213-384-3	Sequence 3, Appl1
13	713	66.6	231	US-09-013-881-7	Sequence 7, Appl1
14	245	22.9	218	US-09-216-001-4	Sequence 4, Appl1
15	245	22.9	218	US-08-878-862-4	Sequence 4, Appl1
16	227.5	21.3	237	US-09-216-001-1	Sequence 1, Appl1
17	227.5	21.3	237	US-08-878-862-1	Sequence 1, Appl1
18	81.5	7.6	358	US-08-034-650-10	Sequence 10, Appl1
19	81.5	7.6	358	US-08-449-015-10	Sequence 10, Appl1
20	81.5	7.6	1005	US-09-770-170-4	Sequence 4, Appl1
21	79	7.4	400	US-09-390-234-19	Sequence 19, Appl1
22	79	7.4	400	US-09-390-234-22	Sequence 22, Appl1
23	79	7.4	560	US-08-756-317-8	Sequence 8, Appl1
24	78	7.3	267	US-08-935-263-10	Sequence 10, Appl1
25	78	7.3	267	US-09-594-185-10	Sequence 10, Appl1
26	77.5	7.2	252	US-09-134-001C-5644	Sequence 5644, Ap
27	77	7.2	1719	US-08-459-568-4	Sequence 4, Appl1

28	77	7.2	1719	2	US-08-399-411-4	Sequence 4, Appl1
29	77	7.2	1719	3	US-08-516-859A-4	Sequence 4, Appl1
30	77	7.2	1719	4	US-09-586-472-4	Sequence 4, Appl1
31	77	7.2	1719	4	US-09-528-706-4	Sequence 4, Appl1
32	76.5	7.1	256	4	US-09-355-166-2	Sequence 2, Appl1
33	76	7.1	353	3	US-08-978-589A-2	Sequence 2, Appl1
34	76	7.1	895	4	US-08-827-962-19	Sequence 19, Appl1
35	76	7.1	895	4	US-08-827-962-21	Sequence 21, Appl1
36	76	7.1	1162	4	US-08-827-962-15	Sequence 15, Appl1
37	76	7.1	1162	4	US-08-827-962-20	Sequence 20, Appl1
38	76	7.1	1162	4	US-08-803-346-1	Sequence 1, Appl1
39	75.5	7.1	346	2	US-08-602-359A-34	Sequence 34, Appl1
40	75.5	7.1	363	4	US-09-336-601-1	Sequence 1, Appl1
41	75.5	7.1	373	4	US-09-039-198A-14	Sequence 14, Appl1
42	75.5	7.1	373	4	US-09-039-198A-15	Sequence 15, Appl1
43	75.5	7.1	373	4	US-08-877-599-14	Sequence 14, Appl1
44	75.5	7.1	373	4	US-08-877-599-15	Sequence 15, Appl1
45	75.5	7.1	373	4	US-09-267-574-14	Sequence 14, Appl1

ALIGNMENTS

```
RESULT 1
US-08-844-120-1
; Sequence 1, Application US/08844120
; Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Puri
ATTORNEY/AGENT INFORMATION: MURRY, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 267650
US-08-844-120-1
Query Match 99.8%; Score 1068; DB 2; Length 208;
Best local Similarity 100.0%; Pred. No. 6,8e-118;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGNNSTPLPAIVPARKATAVIFLHGIGDGPVRYPTLNNNVAMPMSWFDIIGLSPDS 60
Db 1 MCGNNSTPLPAIVPARKATAVIFLHGIGDGPVRYPTLNNNVAMPMSWFDIIGLSPDS 60
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QY 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSOGALSLYTALTTOOKLAGVTAL 120
DB 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSOGALSLYTALTTOOKLAGVTAL 120
QY 121 SFLPLRXSFPOGPIGANGNDISILQCHGDDPLVPLMFGLTYVEKLTLYNPANVTFTK 180
DB 121 SFLPLRXSFPOGPIGANGNDISILQCHGDDPLVPLMFGLTYVEKLTLYNPANVTFTK 180
QY 181 YEGMMHSSCOQEMDMVKQFIDKLLPPI 208
DB 181 YEGMMHSSCOQEMDMVKQFIDKLLPPI 208

RESULT 2
US-09-213-394-1
; Sequence 1, Application US/09213394
; Patent No. 6319701
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,394
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0535
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT19
; CLONE: 2676650
; US-09-213-394-1

Query Match 99.8%; Score 1068; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 6,8e-118;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGVPKRVTLNNNVAMPSPFDIIGLSPDS 60
DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGVPKRVTLNNNVAMPSPFDIIGLSPDS 60
QY 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSOGALSLYTALTTOOKLAGVTAL 120
DB 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSOGALSLYTALTTOOKLAGVTAL 120
QY 121 SFLPLRXSFPOGPIGANGNDISILQCHGDDPLVPLMFGLTYVEKLTLYNPANVTFTK 180
DB 121 SFLPLRXSFPOGPIGANGNDISILQCHGDDPLVPLMFGLTYVEKLTLYNPANVTFTK 180

DB 121 SFLPLRXSFPOGPIGANGNDISILQCHGDDPLVPLMFGLTYVEKLTLYNPANVTFTK 180
QY 181 YEGMMHSSCOQEMDMVKQFIDKLLPPI 208
DB 181 YEGMMHSSCOQEMDMVKQFIDKLLPPI 208

RESULT 3
US-09-022-940-1
; Sequence 1, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-022-940-1

Query Match 98.6%; Score 1055; DB 2; Length 207;
Best Local Similarity 99.5%; Pred. No. 2,3e-116;
Matches 206; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGVPKRVTLNNNVAMPSPFDIIGLSPDS 60
DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGVPKRVTLNNNVAMPSPFDIIGLSPDS 60
QY 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSOGALSLYTALTTOOKLAGVTAL 120
DB 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSOGALSLYTALTTOOKLAGVTAL 120
QY 121 SFLPLRXSFPOGPIGANGNDISILQCHGDDPLVPLMFGLTYVEKLTLYNPANVTFTK 180
DB 121 SFLPLRXSFPOGPIGANGNDISILQCHGDDPLVPLMFGLTYVEKLTLYNPANVTFTK 180
QY 181 YEGMMHSSCOQEMDMVKQFIDKLLPPI 207
DB 181 YEGMMHSSCOQEMDMVKQFIDKLLPPI 207

RESULT 4


```

US-09-216-386-1
; Sequence 1, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216.386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022.940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-216-386-1

Query Match          98.6%; Score 1055; DB 3; Length 207;
Best Local Similarity 99.5%; Pred. No. 2.3e-116;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTGVPVTLNMNVAMPSPWDIIGLSPDS 60
DB 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTGVPVTLNMNVAMPSPWDIIGLSPDS 60
QY 61 QDESGIRKQAEENIKALIDQEVKNGIPSNRIILGFSOGGALSYTALTTOOKLAGVTAL 120
DB 61 QDESGIRKQAEENIKALIDQEVKNGIPSNRIILGFSOGGALSYTALTTOOKLAGVTAL 120
QY 121 SFLPLRXSFPGPIGANGRDISILQCHGDDPLVPLMFGSLTVEKLTIVNPANVTFKT 180
DB 121 SFLPLRXSFPGPIGANGRDISILQCHGDDPLVPLMFGSLTVEKLTIVNPANVTFKT 180
QY 181 YEGMHSSCOQEMDMVKOFIDKLPPID 207
DB 181 YEGMHSSCOQEMDMVKOFIDKLPPID 207

RESULT 5
US-09-022-940-3
; Sequence 3, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022.940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-022-940-3

Query Match          96.6%; Score 1034; DB 2; Length 230;
Best Local Similarity 89.1%; Pred. No. 8.2e-114;
Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTG-----PVPR 38
DB 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTG-----PVPR 38
QY 39 VTLNMNVAMPSPWDIIGLSPDSQDESGIRKQAEENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 61 VTLNMNVAMPSPWDIIGLSPDSQDESGIRKQAEENIKALIDQEVKNGIPSNRIILGFSQ 120
QY 99 GALSILYALTTOOKLAGVTALSFPLPLRXSFPGPIGANGRDISILQCHGDDPLVPLM 158
DB 121 GALSILYALTTOOKLAGVTALSCWPLPLRXSFPGPIGANGRDISILQCHGDDPLVPLM 180
QY 159 FGSILTVEKLTIVNPANVTFKTEGMMHSSCOQEMDMVKOFIDKLPPID 208
DB 181 FGSILTVEKLTIVNPANVTFKTEGMMHSSCOQEMDMVKOFIDKLPPID 230

RESULT 6
US-09-216-386-3
; Sequence 3, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-3

Query Match 96.6%; Score 1034; DB 3; Length 230;
Best Local Similarity 89.1%; Pred. No. 8.2e-114;
Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDPTG-----PYRP 38
||||| :|||:|||||
DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDPTGHNAAEFAGIRSHIKYICPHAPVP 60
||||| :|||:|||||
QY 39 VTLMNVAMPSPWFIDIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 98
||||| :|||:|||||
DB 61 VTLMNVAMPSPWFIDIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 120
||||| :|||:|||||
QY 99 GGALSLYTLTQOKLAGVTALSFLLPLRXSPQGPIGGANDISILQCHGDCDPLVPLM 158
||||| :|||:|||||
DB 121 GGALSLYTLTQOKLAGVTALSCWPLRLRASFPQGPIGGANDISILQCHGDCDPLVPLM 180
||||| :|||:|||||
QY 159 FGSITVEKLTLPNPAVNTFKTEYEGMMHSSCOQEMMDVKQFIDKLLPID 208
||||| :|||:|||||
DB 181 FGSITVEKLTLPNPAVNTFKTEYEGMMHSSCOQEMMDVKQFIDKLLPID 230
||||| :|||:|||||

RESULT 7
US-08-844-120-3
Sequence 3, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244
US-08-844-120-3

Query Match 89.5%; Score 958; DB 2; Length 230;
Best Local Similarity 81.7%; Pred. No. 7.5e-105;
Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDPTG-----PYRP 38
||||| :|||:|||||
DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDPTGHNAAEFAGIRSHIKYICPHAPVP 60
||||| :|||:|||||
QY 39 VTLMNVAMPSPWFIDIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 98
||||| :|||:|||||
DB 61 VTLMNVAMPSPWFIDIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 120
||||| :|||:|||||
QY 99 GGALSLYTLTQOKLAGVTALSFLLPLRXSPQGPIGGANDISILQCHGDCDPLVPLM 158
||||| :|||:|||||
DB 121 GGALSLYTLTQOKLAGVTALSCWPLRLRASFPQGPIGGANDISILQCHGDCDPLVPLM 180
||||| :|||:|||||
QY 159 FGSITVEKLTLPNPAVNTFKTEYEGMMHSSCOQEMMDVKQFIDKLLPID 208
||||| :|||:|||||
DB 181 FGSITVEKLTLPNPAVNTFKTEYEGMMHSSCOQEMMDVKQFIDKLLPID 230
||||| :|||:|||||

RESULT 8
US-09-022-940-5
Sequence 5, Application US/09022940
Patent No. 5965423
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,940
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 230 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-022-940-5

Query Match 89.5%; Score 958; DB 2; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38
 Db 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTGHEAFAGIKSHIKYICPHAPVP 60
 QY 39 VTLNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 61 VTLNNSMMPSPWFDIIGLSPDSQDESGIKQAETVAKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGALSLYALTTOOKLAGVTAFLPLRXSPQPGTIGGANDRISILQCHGDCDPLVPLM 158
 Db 121 GGALSLYALTTOOKLAGVTAFLSCWPLRASFSGPTINSANRDISVLQCHGDCDPLVPLM 180
 QY 159 FGSLLVEKLTIVNPANVTFTYEGMMHSSCOQEMMDVKYFDKLLPPID 208
 Db 181 FGSLLVEKLTIVNPANVTFTYEGMMHSSCOQEMMDVKYFDKLLPPID 230

RESULT 9

US-09-216-001-3
 Sequence 3, Application US/09216001
 Patent No. 6004792

GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Shah, Purvi
 APPLICANT: Corley, Neil C.
 APPLICANT: Murry, Lynn E.
 TITLE OF INVENTION: NEW HUMAN LYOPHOSPHOLIPASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESS: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/216,001
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/878,862
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0329 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 230 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank

CLONE: 1552244
 US-09-216-001-3

Query Match 89.5%; Score 958; DB 3; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38
 Db 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTGHEAFAGIKSHIKYICPHAPVP 60
 QY 39 VTLNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 61 VTLNNSMMPSPWFDIIGLSPDSQDESGIKQAETVAKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGALSLYALTTOOKLAGVTAFLPLRXSPQPGTIGGANDRISILQCHGDCDPLVPLM 158
 Db 121 GGALSLYALTTOOKLAGVTAFLSCWPLRASFSGPTINSANRDISVLQCHGDCDPLVPLM 180
 QY 159 FGSLLVEKLTIVNPANVTFTYEGMMHSSCOQEMMDVKYFDKLLPPID 208
 Db 181 FGSLLVEKLTIVNPANVTFTYEGMMHSSCOQEMMDVKYFDKLLPPID 230

RESULT 10

US-09-216-386-5
 Sequence 5, Application US/09216386
 Patent No. 6033561

GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Shah, Purvi
 APPLICANT: Murry, Lynn E.
 TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/216,386
 FILING DATE:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/022,940
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 230 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-216-386-5

Query Match 89.5%; Score 958; DB 3; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;
 QY 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38
 Db 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38

Db 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDGTGHWAEAFAGIKSSHITKICPHAPVMP 60
 QY 39 VTLNMVAMPSPWFIDTIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 61 VTLNMSMAMPSPWFIDTIGLSPDSQEDSGIKQAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGALSLYLTALTTOOKLAGVTALSFLLPLRXSPGPIGGANRDISILOCHGDCDPLVPLM 158
 Db 121 GGALSLYLTALTTOOKLAGVTALSCWPLRASFSGQPIINSANRDISVLOCHGDCDPLVPLM 180
 QY 159 FGSILVEKLKTLVNPANVTFTKYEKGMMHSSCOQEMMDVYKQFIDKLPLPID 208
 Db 181 FGSILVEKLKTLVNPANVTFTKYEKGMMHSSCOQEMMDVYKQFIDKLPLPID 230

RESULT 11

US-08-878-862-3
 ; Sequence 3, Application US/08878862
 ; Patent No. 6143544
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/878,862
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0329 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 230 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1552244
 ; US-08-878-862-3
 Query Match 89.5%; Score 958; DB 4; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;
 QY 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDGTG-----PVP 38
 Db 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDGTGHWAEAFAGIKSSHITKICPHAPVMP 60
 QY 39 VTLNMVAMPSPWFIDTIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98

Db 61 VTLNMSMAMPSPWFIDTIGLSPDSQEDSGIKQAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGALSLYLTALTTOOKLAGVTALSFLLPLRXSPGPIGGANRDISILOCHGDCDPLVPLM 158
 Db 121 GGALSLYLTALTTOOKLAGVTALSCWPLRASFSGQPIINSANRDISVLOCHGDCDPLVPLM 180
 QY 159 FGSILVEKLKTLVNPANVTFTKYEKGMMHSSCOQEMMDVYKQFIDKLPLPID 208
 Db 181 FGSILVEKLKTLVNPANVTFTKYEKGMMHSSCOQEMMDVYKQFIDKLPLPID 230

RESULT 12

US-09-213-394-3
 ; Sequence 3, Application US/09213394
 ; Patent No. 6319701
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Murry, Lynn E.
 ; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/213,394
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/844,120
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0269 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 230 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 552244
 ; US-09-213-394-3
 Query Match 89.5%; Score 958; DB 4; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;
 QY 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDGTG-----PVP 38
 Db 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDGTGHWAEAFAGIKSSHITKICPHAPVMP 60
 QY 39 VTLNMVAMPSPWFIDTIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 61 VTLNMSMAMPSPWFIDTIGLSPDSQEDSGIKQAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGALSLYLTALTTOOKLAGVTALSFLLPLRXSPGPIGGANRDISILOCHGDCDPLVPLM 158
 Db 121 GGALSLYLTALTTOOKLAGVTALSCWPLRASFSGQPIINSANRDISVLOCHGDCDPLVPLM 180

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QY 159 FGSITVEKLTLPNPAVTFKTYEGMMHSSCOQEMNDVKQFIDKLLPPID 208
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Db 181 FGSITVERLKGVPNPANVTFKTYEGMMHSSCOQEMNDVKYFIDKLLPPID 230
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RESULT 13

US-09-013-881-7
Sequence 7, Application US/09013881
Patent No. 6132964
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Ial, Pirelli
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Giegler, Karl J.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0470 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLANOTO2
CLONE: 2768301
US-09-013-881-7

	Query Match:	66.6%;	Score	713;	DB	4;	Length	231.
	Best Local Similarity	60.8%;	Pred.	No.	6e-76;			
	Matches	141;	Conservative	28;	Mismatches	37;	Indels	26;
					Gaps			3.
OY	1	MCGNMSTPL--PAIVPARRATAAVIFLHGLDGTG-----	-P	35				
Db	1	MGNTMSVPLLTDAATVSGARETAIAFLHGLDGTGSMWALSTIRLPHVKYICPHAP		60				
OY	36	VRRPTLLMANVAMPSSWDITIGLSPSDOESDGKAAENIKKLIDQEVKNKGPSNRILLGG	95					
		:						
Db	61	RIPLTLMKKVMSPMDLGMGLSPDAPEDEAGICKAKAENIKALKIHEEMKNGIPANRITVLG	120					
		:						
OY	96	FSOGGALSTKTALTTOOKLAGVTALSTFLPLRXSPGPGRIGGARNDRTSLIOCHGDGDDPY	155					
Db	121	FSOGGALSTLTATTCPIPLAGIIVALSCWLPRLRAPQAANSO-KDLATIQCHEELDPNV	179					

QY 156 PLMGSLTYEKLKLVNPAVTFRTYEGMMHSSCOQEMDMVKQFIDKLLPPI 207
 180 PVREGALTAEKLRSVTPARVQFRTYPGVMHSSCPQEMAAYKEFLLEKLLPV 231

RESULT 14

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US-09-216-001-4
Sequence 4, Application US/09216001
Patent No. 6004792
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NEW HUMAN LYSPHOSPHOLIPASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,001
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,862
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0329 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ. ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 244501
US-09-216-001-4

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[illegible]

Job time : 58 secs

RESULT 15

US-08-878-862-4

; Sequence 4, Application US/08878862

; Patent No. 6143544

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; APPLICANT: Murry, Lynn E.

; TITLE OF INVENTION: NEW HUMAN LYOPHOSPHOLIPASE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/878,862

; FILING DATE: Herewith

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0329 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 244501

; US-08-878-862-4

Query Match 22.9%; Score 245; DB 4; Length 218;

Best Local Similarity 33.0%; Pred. No. 8.8e-21; Indels 32; Gaps 6;

Matches 70; Conservative 30; Mismatches 80;

QY 11 PAIYPAARKATAAVIFHGLG-----DTGPVRYPTLNMNVA 46

Db 4 PLIIQPAKPADACVYIWHGICADRYDEMRYAALQESLITRVLQAQPRPTINGCYE 63

QY 47 MPWFIDILSPDSQDEDSIGKQAEENIKALIDQEVKNGIPSNRIILGFSOGALSLEYT 106

Db 64 MPWFYDIKAMSPARSISLELEYSAMKVVTDLEAQKRTGIGASRIPLAGFSOGAVVFHT 123

QY 107 A-LTQOKLAGVTALSLFLPLKRSF-PQGPFGANDISITLQCHGCDPLVPLMFSGLTY 164

Db 124 AFINMOGLGVIALSTYAP--TFGDELELSASQORIPALCLHGQYDDVYQANMGRSAF 180

QY 165 EKLKTLVNPANVTFTKTEGMMHSSCOEMMDV 196

Db 181 EHLKS--RGVYTWQETP-MGHEVLPQELHDI 209

Search completed: January 19, 2003, 03:25:56

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 19, 2003, 03:20:15 : Search time 75 Seconds
(without alignments)
55.130 Million cell updates/sec

Title: US-09-988-982-1
Perfect score: 1070
Sequence: 1 MCGNNMSTPLPAIVPARKA.....COQEMMDVKQIDKLPLPID 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 120991 segs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications-AA:
1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1068	99.8	208	10 US-09-988-982-1	Sequence 1, Appli
2	1034	96.6	263	10 US-09-925-299-991	Sequence 991, App
3	958	89.5	230	10 US-09-988-982-3	Sequence 3, Appli
4	521.5	48.7	236	9 US-09-934-392-4	Sequence 4, Appli
5	89.5	8.4	219	10 US-09-791-171-14	Sequence 14, Appli
6	86	8.0	197	10 US-09-815-242-5457	Sequence 5457, Ap
7	86	8.0	198	10 US-09-815-242-16680	Sequence 12680, A
8	81	7.6	226	10 US-09-791-171-52	Sequence 52, Appli
9	81	7.6	322	10 US-09-815-242-11790	Sequence 11790, A
10	79.5	7.4	308	9 US-09-738-626-3637	Sequence 3637, Ap
11	79	7.4	217	10 US-09-791-171-10	Sequence 10, Appli
12	79	7.4	262	10 US-09-791-171-56	Sequence 56, Appli
13	78	7.3	267	12 US-10-033-078-10	Sequence 10, Appli
14	77	7.2	310	9 US-09-934-392-2	Sequence 2, Appli
15	76.5	7.1	256	10 US-09-950-368-2	Sequence 2, Appli
16	75.5	7.1	346	9 US-10-027-805-34	Sequence 34, Appli
17	75	7.0	891	9 US-09-976-059-18	Sequence 18, Appli
18	74.5	7.0	285	9 US-10-051-643-197	Sequence 197, App
19	74.5	7.0	308	10 US-09-999-162-2	Sequence 2, Appli

20	74.5	7.0	346	10 US-09-903-410-34	Sequence 34, Appli
21	74	6.9	700	10 US-09-840-707A-9	Sequence 9, Appli
22	74	6.9	700	10 US-09-768-877-23	Sequence 23, Appli
23	73.5	6.9	297	9 US-10-027-805-37	Sequence 37, Appli
24	73.5	6.9	297	10 US-09-903-410-37	Sequence 37, Appli
25	73.5	6.9	354	10 US-09-999-162-14	Sequence 14, Appli
26	73	6.8	601	10 US-09-815-242-5070	Sequence 5070, Ap
27	72.5	6.8	271	9 US-09-738-626-6380	Sequence 6380, Ap
28	72.5	6.8	331	9 US-09-738-626-3832	Sequence 3832, Ap
29	72	6.7	200	10 US-09-815-242-10705	Sequence 10705, A
30	72	6.7	1053	10 US-09-815-242-5136	Sequence 5136, Ap
31	69.5	6.5	262	9 US-10-027-805-38	Sequence 38, Appli
32	69.5	6.5	262	10 US-09-903-410-38	Sequence 38, Appli
33	69.5	6.5	416	10 US-09-805-848A-2	Sequence 2, Appli
34	69.5	6.5	416	10 US-09-805-848A-4	Sequence 4, Appli
35	69.5	6.5	655	9 US-10-117-641-36	Sequence 36, Appli
36	69.5	6.5	1062	10 US-09-815-242-5111	Sequence 5111, Ap
37	69	6.4	300	10 US-09-794-960-5	Sequence 5, Appli
38	68.5	6.4	167	9 US-10-051-643-112	Sequence 112, App
39	68.5	6.4	167	9 US-09-880-505-112	Sequence 112, App
40	68.5	6.4	232	10 US-09-896-578-4	Sequence 4, Appli
41	68.5	6.4	247	9 US-09-738-626-6438	Sequence 6438, Ap
42	68.5	6.4	271	9 US-09-976-059-10	Sequence 10, Appli
43	68.5	6.4	748	9 US-10-051-643-154	Sequence 154, App
44	68.5	6.4	748	9 US-09-880-505-154	Sequence 154, App
45	68	6.4	229	10 US-09-879-957-221	Sequence 221, App

ALIGNMENTS

RESULT 1
US-09-988-982-1
Sequence 1, Application US/09988982
Patent No. US20020081699A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-NO. US20020081699A1-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
FAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: KIDNOC19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-988-982-1

Query Match 99.8%; Score 1068; DB 10; Length 208;
Best Local Similarity 100.0%; Pred. No. 1,7e-108;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGNNSTPLPAIVPAARATAAIVFLHGLGDTGPRPTLVNNAVAMPSPMDIIGLSPDS 60
DB 1 MCGNNSTPLPAIVPAARATAAIVFLHGLGDTGPRPTLVNNAVAMPSPMDIIGLSPDS 60
QY 61 QEDDSGKQAEENIKALIDQEVKNGIPSNRIILGFSQGALSIXTALTTOOKLAGVTAL 120
DB 61 QEDDSGKQAEENIKALIDQEVKNGIPSNRIILGFSQGALSIXTALTTOOKLAGVTAL 120
QY 121 SFLLPLRXSPGPGPIGANDRDISILQCHGDCDPLVPLMGSLTVEKTKLVNNAVTEKT 180
DB 121 SFLLPLRXSPGPGPIGANDRDISILQCHGDCDPLVPLMGSLTVEKTKLVNNAVTEKT 180
QY 181 YEGMHSSCOQEMMDVKQFIDKLLPPID 208
DB 181 YEGMHSSCOQEMMDVKQFIDKLLPPID 208

RESULT 2

US-09-925-299-991
Sequence 991, Application US/09925299
Patent No. US20020055627A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 991
LENGTH: 263
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-991

Query Match 96.6%; Score 1034; DB 10; Length 263;
Best Local Similarity 89.1%; Pred. No. 1.2e-104;
Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARATAAIVFLHGLGDTG-----PVRP 38
DB 34 MCGNNSTPLPAIVPAARATAAIVFLHGLGDTGHGMAEAFAGIKSSHIIKTCPPHAPVR 93
QY 39 VTLNNAVAMPSPMDIIGLSPDSQEDDSGKQAEENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 94 VTLNNAVAMPSPMDIIGLSPDSQEDDSGKQAEENIKALIDQEVKNGIPSNRIILGFSQ 153
QY 99 GGALSIXTALTTOOKLAGVTALSFLLPLRXSPGPGPIGANDRDISILQCHGDCDPLVPLM 158
DB 154 GGALSIXTALTTOOKLAGVTALSCWLPRLASFSQPIGANDRDISILQCHGDCDPLVPLM 213
QY 159 FGSILTVEKTKLVNNAVTEKTYEGMHSSCOQEMMDVKQFIDKLLPPID 208
DB 214 FGSILTVEKTKLVNNAVTEKTYEGMHSSCOQEMMDVKQFIDKLLPPID 263

RESULT 3

US-09-988-982-3
Sequence 3, Application US/09988982
Patent No. US20020081699A1

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Murry, Lynn E.

TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-No. US20020081699A1-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-988-982-3

Query Match 89.5%; Score 958; DB 10; Length 230;
Best Local Similarity 81.7%; Pred. No. 1.8e-96;
Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARATAAIVFLHGLGDTG-----PVRP 38
DB 1 MCGNNSTPLPAIVPAARATAAIVFLHGLGDTGHGMAEAFAGIKSSHIIKTCPPHAPVR 60
QY 39 VTLNNAVAMPSPMDIIGLSPDSQEDDSGKQAEENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 61 VTLNNAVAMPSPMDIIGLSPDSQEDDSGKQAEATVATLIDQEVKNGIPSNRIILGFSQ 120
QY 99 GGALSIXTALTTOOKLAGVTALSFLLPLRXSPGPGPIGANDRDISILQCHGDCDPLVPLM 158
DB 121 GGALSIXTALTTOOKLAGVTALSCWLPRLASFSQPIGANDRDISILQCHGDCDPLVPLM 180
QY 159 FGSILTVEKTKLVNNAVTEKTYEGMHSSCOQEMMDVKQFIDKLLPPID 208
DB 181 FGSILTVEKTKLVNNAVTEKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 4

US-09-934-392-4
Sequence 4, Application US/09934392
Patent No. US20020155497A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38618, A NOVEL HUMAN ALPHA/BETA
HYDROLASE FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-082001


```

FILE REFERENCE: 670001-2002..1
CURRENT APPLICATION NUMBER: US/09/791.171
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 226
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-791-171-52

Query Match          7.6%, Score 81; DB: 10; Length 226;
Best Local Similarity 23.9%, Pred. No. 0.29;
Matches    44; Conservative   21; Mismatches   57; Indels    62; Gaps    10;

OY      11 PAIYAARKA--TAIVIFLH-----GAGDGPVAPVTILNM-----NYAMPSWEDI 53
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      37 PALAPPASAGCPDAVVVARRGTEPPGLGRGQAFVSSIRQOTNKSIGTYGVNYRANGDF 96
OY      54 IGLSPDSODESGIKQAENKALIDOEYKNKIPSNRIILGGFSOGGA-LSLYTALTTOO 112
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      97 LAAR-----DGANDASDHI-----QQMASACRAFRVLVGYSQGAVIDIVTA----- 139
OY      113 KLAGVTALSFLPLRXSF-----PGPIGGANROISIIQCHGDCLPYPLMFG 160
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      140 --APLPGLGTPTLPADDDHTATATALPFGNPGRAGGL-----MSALTP-QFG 184
OY      161 SLTV 164
           |::|
DB      185 SKTI 188

RESULT 9
US-09-815-242-11790
Sequence 11790, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes In
TITILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815.242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308

```

; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11790
; LENGTH: 322
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11790

Query Match 7.6%; Score 81; DB 10; Length 322;
Best Local Similarity 21.3%; Pred. No. 0.47;
Matches 37; Conservative 33; Mismatches 72; Indels 32; Gaps 7;

QY 13 IYPAARKATAAVFIHG-AGDTGVPVPT-----LNMMVAMPWFIDIGSPDSQ 61
DB 59 VPPGSEGAFLVLVHLSGSGDQGMRIISGYGFDRLAAGEFLVAYPDGFE--GIMNDCR 116
DB 62 E-----DESGIKOAEENIKALIDQEVKNGIPSRILIGFSGGALSTYALT 110
DB 117 KASYSARLRDVEDVAFLRA--LVARLAQEYR--VDSQRYVAGYSGNGQAFRLAABA 171
QY 111 QOKLAGVTALFLPLRXSPGPIGANDISIIQCHDCDPLVPLMGSLTV 164
DB 172 PGLPAAIAAVALSLPTTGNDACRPV--BRPTAALINSTRDPIINPYLGKVS 222

RESULT 10

US-09-738-626-3637
; Sequence 3637, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIRO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3637
; LENGTH: 308
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3637

Query Match 7.4%; Score 79.5; DB 9; Length 308;
Best Local Similarity 26.9%; Pred. No. 0.65;
Matches 29; Conservative 20; Mismatches 38; Indels 21; Gaps 4;

QY 24 VIFHLGDTGVPVPTLMM-----NVAMPWFIDIGSPD-----SQDESGIKOA 70
DB 74 LVYFHGGGSGC---TLMDIATVHSLVGLP-----ITLSVDYRLAPAFHPPAIDA 125
QY 71 AENIKALIDQEVKNGIPSRILIGFSGGALSTYALTTOOKLAGVT 118
DB 126 FAVVASVLVGSGLSDTSRAVIGDSAGNIAVTAQDLRRAGVST 173

RESULT 11

US-09-791-171-10
; Sequence 10, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WEIDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 217
; TYPE: PRF
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-10

Query Match 7.4%; Score 79; DB 10; Length 217;
Best Local Similarity 25.4%; Pred. No. 0.45;
Matches 46; Conservative 24; Mismatches 59; Indels 52; Gaps 10;

QY 6 MSTPLPAI-VPARKAT-----AAVIFLH-----GIDGTGVPVPTLMMNVAMPWF 51
DB 14 VATTALVSAFAGGAAHADPCSDIAVFAFGTHQASGLGVGAFYDSLTSOVGGRS-- 71
QY 52 DIIGL---SPDSODESGIKOAEENIKALIDQEVKNGIPSRILIGFSGG----- 99
DB 72 --IGYAVNYASDDYRASASNGSDASAHQRTVAS--CPRTRYLGGYSGGATVIDLST 128
QY 100 -----GALSLYALT--QOKLAGVTALFLPLRXS-----FPQGPV--GGA 138
DB 129 SAMPAAVADHVAVALGEPSSGFSMLMGSGSLPTIGPLYSKTNILCAPDDPCTGGG 188
QY 139 N 139
DB 189 N 189

RESULT 12

US-09-791-171-56
; Sequence 56, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WEIDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739

```

; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 56
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-56

```

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Query Match
Best Local Similarity 72.4%; Score 79; DB 10; Length 262;
Matches 44; Conservative 26; Mismatches 53; Indels 76; Gaps 10;

```

```

QY 23 AVIFLHIG-----DTGPRVPTLNNVAMPSPFDITIGS-PDSQDESGIK---- 68
DB 24 AVVLLIAGAVTVPVAFADGCPDAEYTFARGTGPICGVQAFVDSLQGTGMEIGVY 83
QY 69 -----QAAENIKALIDQEVKNGIPSNRIILGFSOGGALSITALT 110
DB 84 PVNVAASHLQIHGGDAGANDAIISHIKSM-----ASSCPNTKLVLGGYSOGA-----TV 130
QY 111 QOKLAGVT--ALSFLLPLRKSF-----PGGPIGAGNDISILQCHGDCDPLVP 156
DB 131 IDIYAGVPLGSIISFGSPRAIYANNAVAVFGNPSNRAGSSLSLS-----P 178
QY 157 LMFSGSLTVEKLTIVNPAN 175
DB 179 L-FGSKAID---LCNPTD 192

```

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RESULT 13
US-10-033-078-10
; Sequence 10, Application US/10033078
; Patent No. US20020123109A1
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuya
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/10/033,078
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 09/594,185
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: EP 96115540.5
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-10-033-078-10

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```

Query Match
Best Local Similarity 7.3%; Score 78; DB 12; Length 267;
Matches 46; Conservative 33; Mismatches 57; Indels 78; Gaps 11;

```

```

QY 27 LHGIDTGPVPRVTLNNVAMP--SW-----FDLIGSPDSQ--EDESCIK 68
DB 15 VHGGD-----PLLLINGLGNLSIMHRTVPTLAKRKRVIVFDDRGGKSSKPEQPSYS 69
QY 69 QAAENIKALIDQEVKNGIPSNRIILGFSOGGALSITALTTOOKL-----ACVTA 119

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DB 70 MAEDARAVLD-----AVSVDASAHYGISMGMIARLAIATYPERVRSIVLCTTAGGT 124
QY 120 -----LSFLPLRKSFPQGPICGANRDISILOCHGDCDPLVPLMFSGSLTVEKLTIVN 172
DB 125 HIQPSPEISTLWVSRAS-----LTGSPRDNAML-----AAPIVYSOAFLEK----- 165
QY 173 PANVTFKTEGMMHSSCOQEMMDVKQOFIDKLPP 206
DB 166 -----HPELIDQ--DIQKRIDEITPP 184

```

```

RESULT 14
US-09-934-392-2
; Sequence 2, Application US/09934392
; Patent No. US20020155497A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38618, A NOVEL HUMAN ALPHA/BETA
; FILE REFERENCE: 10448-082001
; CURRENT APPLICATION NUMBER: US/09/934,392
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/226,737
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-392-2

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Query Match
Best Local Similarity 7.2%; Score 77; DB 9; Length 310;
Matches 57; Conservative 33; Mismatches 91; Indels 52; Gaps 13;

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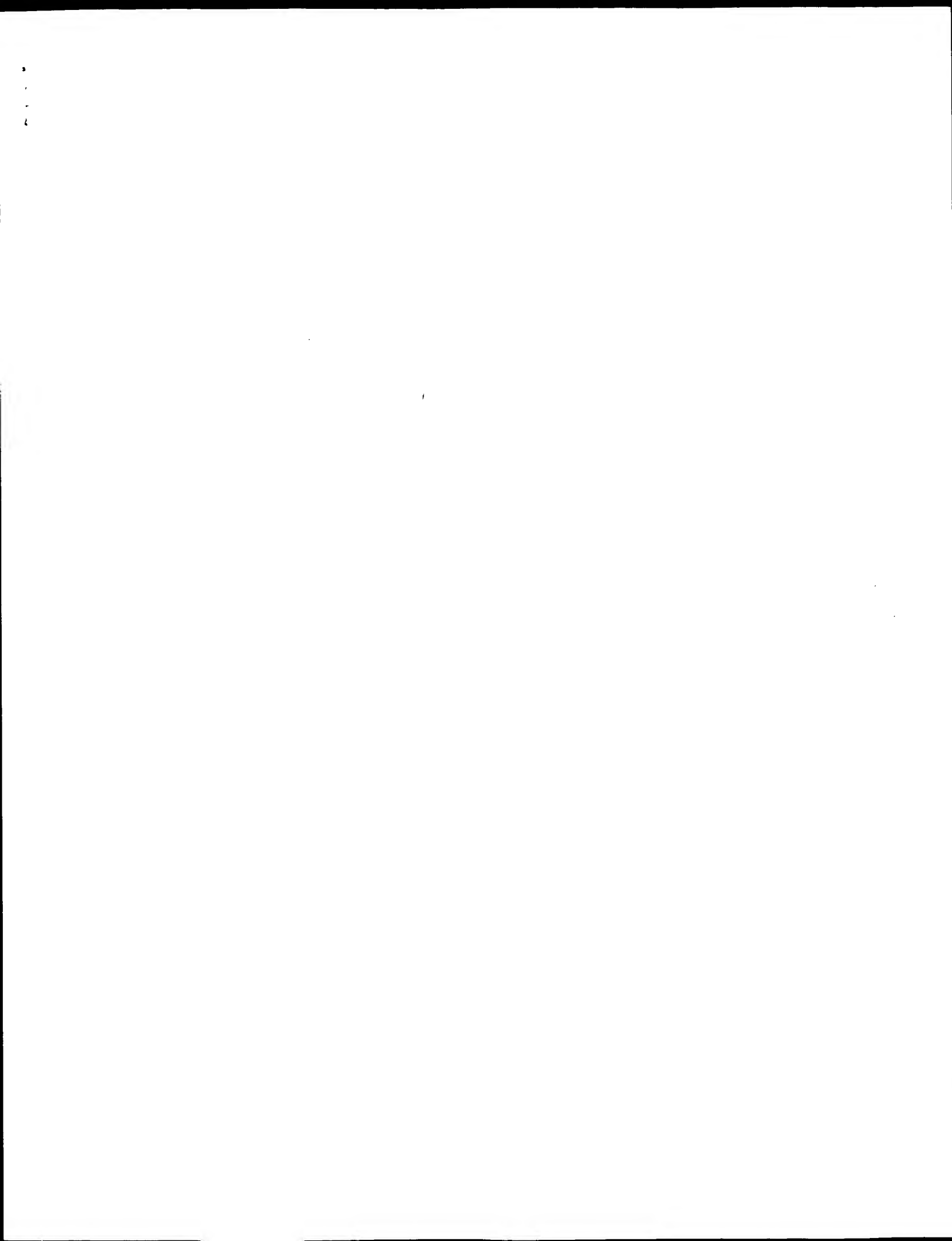
QY 3 GNNMSTPLPAIYPAARKATAAVIFLHIGL-DTGPRV-----TLNNVAMPSPFDITIG 55
DB 96 GNRVSCMYRCVPGAR---YTVLFSGHNAVVDLGOMSFYIGSLRHCNIFS---YDSCG 149
QY 56 LSPDSQDESGIKQAENIKALIDQ-----EVKNGIPSNRIILGFSOG----- 99
DB 150 YGASSG-----RPSERNLYADIDAAMQALRRYGISPSDITLYGOSIGTVPYDLASRY 203
QY 100 --GALSITALTTOOKLA-CYTAISFLPLRKSFPQGPICGANRDIS--ILOCHGDCDPLV 155
DB 204 ECAAVVLSHPLTSGMRVAFPDTRKTYCF--DAFPN--LEKSKITSPVLIITGTEDEVI 258
QY 156 PLMFSGSLTVEKLTIVNPANVTFKTEGMMHSSCO---QEMMDVKQOFIDKLPP 205
DB 259 DPSHGIALYERCKAVERPLMV-----EGAGHNDIELYSYLERLRLRFSIQELP 306

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```

RESULT 15
US-09-950-368-2
; Sequence 2, Application US/09950368
; Patent No. US20020061580A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolyase-Fold Enzymes
; FILE REFERENCE: GC511-BCT
; CURRENT APPLICATION NUMBER: US/09/950,368
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/355,166
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Bacillus
US-09-950-368-2

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 19, 2003, 03:15:41 ; Search time 77 seconds
(without alignments)
259.688 Million cell updates/sec

Title: US-09-988-982-1

Perfect score: 1070

Sequence: 1 MCGNMSTPLPAIVPAPARKA.....COQEMMDVKOFIDKLPLPID 208

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	422.5	39.5	333	2 T23324	hypothetical prote
2	399	37.3	247	2 T52511	related to lysopho
3	318.5	29.8	224	2 T39158	lysophospholipase
4	306	28.6	227	2 S64955	probable membrane
5	273.5	25.6	224	2 H82658	carboxylesterase X
6	248	23.2	215	2 A83163	probable carboxyle
7	245	22.9	218	2 J00277	carboxylesterase (
8	244	22.8	218	2 J00865	esterase A (EC 3.1
9	240.5	22.5	211	2 T04911	hypothetical prote
10	163.5	15.3	204	2 S75304	serine esterase -
11	145.5	13.6	207	2 S43880	esterase - Sp1ru11
12	134	12.5	214	2 AB2195	serine esterase, p
13	128.5	12.0	243	2 D72098	lysophospholipase
14	128.5	12.0	243	2 G86524	probable lysophosp
15	126	11.8	241	2 T39231	hypothetical prote
16	124	11.6	305	2 C96568	hypothetical prote
17	120.5	11.3	305	2 T20470	protein T2E6.14 (f
18	119.5	11.2	166	2 D96518	probable secreted
19	116	10.8	304	2 D86998	probable lpgc prot
20	115	10.7	304	2 C70982	serine esterase, p
21	108	10.1	239	2 F81704	hypothetical prote
22	108	10.1	319	2 AB1334	hypothetical prote
23	105.5	9.9	204	2 F83921	hypothetical prote
24	105.5	9.9	243	2 C95908	hypothetical prote
25	100	9.3	335	2 T20465	hypothetical prote
26	98	9.2	416	2 D70347	cell division prot
27	95.5	8.9	395	2 F72424	hypothetical prote
28	93.5	8.7	200	2 G96550	hypothetical prote
29	93	8.7	378	2 T41456	probable phosphos

30	92.5	8.6	240	2 G91045	hypothetical prote
31	92.5	8.6	240	2 C85890	hypothetical prote
32	91	8.5	197	2 G90055	conserved hypot
33	90.5	8.5	240	2 H65022	hypothetical prote
34	89.5	8.4	219	2 A70734	probable cutinase
35	89.5	8.4	691	2 C72454	hypothetical prote
36	88.5	8.3	215	2 D71634	hypothetical prote
37	88.5	8.3	239	2 A71552	probable lysophosp
38	87.5	8.2	216	2 C97843	serine esterase ho
39	86	8.0	961	2 H86181	hypothetical prote
40	85	7.9	332	2 F96568	probable lipase, 2
41	84.5	7.9	308	2 H70852	probable lipr prot
42	84	7.9	197	2 A96568	hypothetical prote
43	83	7.9	705	1 C1CHH	calpain (EC 3.4.22
44	83	7.8	293	2 S77419	hypothetical prote
45	83	7.8	501	2 C72321	conserved hypot

ALIGNMENTS

RESULT 1
T23324
hypothetical protein K04G2.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23324
R:Gardner, A.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19727
A:Accession: T23324
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-333 (KWL)
A:Cross-references: EMBL:Z75712; PIDN:CAB0042.1; GSPDB:GN00019; CESP:K04G2.5
A:Experimental source: clone K04G2
C:Genetics:
A:Gene: CESP:K04G2.5
A:Map position: 1
A:Introns: 8/1; 54/1; 87/1; 165/2; 263/3; 318/3

Query Match 39.5%; Score 422.5; DB 2; Length 333;
Best local similarity 44.2%; Pred. No. 7.4e-32;
Matches 95; Conservative 23; Mismatches 66; Indels 31; Gaps 5;

QY	11	PAIVPAARKATAVIFLHGIGDTG-----PVPPVTLNNVAM	47
DB	119	PSIVSPRGEHKGTLIFLHGIGDGHGMDAFKTEAKHDKIKFICPHSSRPVTLNNGMFM	178
QY	48	PSMFEDIIGSPDSQEDSESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALSLYTA	107
DB	179	PAWFDFLEGLDPNAGDEQGGIKRATQYVHOLIDAQVAAIGPASTIAVGGFSKGAALATVAG	238
QY	108	LTFTQOKLAGVTALSFLLPRXSPQGPICG--ANRDISLQCHGCDPPLVPIFGSLAYE	165
DB	239	LTPKQALGIVGLSSFFLGRTKRP-----GSFTANNKTPFLFHGHTDDFLVPLQFGMSQ	294
QY	166	KIKTLVNPANVTFTYEGMMHSSCOQEMMDVKOFI	200
DB	295	YIKKF-NP-KVELHTYRGMQHSSCGEMRQVTF	327

RESULT 2
T52511
related to lysophospholipase [imported] - *Neurospora crassa*
N:Alternate names: protein B2J23.70
C:Species: *Neurospora crassa*
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T52511
R:Schulte, U.; Alim, V.; Hohsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, September 2000
A:Reference number: Z26053
A:Accession: T52511

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1624

Query Match 25.6%; Score 273.5; DB 2; Length 224;
Best Local Similarity 32.4%; Pred. No. 4.2e-18;
Matches 67; Conservative 38; Mismatches 71; Indels 31; Gaps 5;

23 AVIFLHGIGDTG-----PVRPVTINMNVAMPSPWDIIGLS 57
16 SVLWHLGIGADGHDMPPIPELVPRHPALREVFPHASVRPTTNGVPMKAWMDLVSEF 75
58 PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALSLVTLTQOKLAGV 117
76 FNGRADAGIEAAVAQVQALMMREQGIGASERLFLAGFSOGGAVVLSIGLRCKASLAGL 135
118 TALSFLLP--LRKSFPGGPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLTLYNPAN 175
136 IALSTYLPDLMAYVTATGGLPGSNAQ--PLFIAGHSDDPVVPLVHGQCAEALRKL--GFA 192
176 VTFKTEGMMHSSCOQEMMDVKOFIDK 202
193 VDMYTYR-MAHQVCQCEIOLADWLER 218

RESULT 6

A83163
probable carboxylesterase PA3859 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83163
C:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Llm,
; Loay, S.; Olson, M.V
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; M0ID:20437337; PMID:10984043
A:Accession: A83163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <STO>
A:Cross-references: GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG07246.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3859

Query Match 23.2%; Score 248; DB 2; Length 215;
Best Local Similarity 32.0%; Pred. No. 9.8e-16;
Matches 73; Conservative 30; Mismatches 87; Indels 34; Gaps 6;

6 MSTPLPAIVPAARKATAAVIFLHGLG-----DTGPRVPVTIL 41
1 MSEPL---IIDAPRADACIIMHGLGADRDYDFKPVAEALQMLVPSFTFLPQAPSAVTV 57
42 MNANVAMPSPWDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGA 101
58 NGCWVMSWMDIILAFSPARAIQEDQLNASADQVIALIDQERAKGIAERILLILGFSOGGA 117
102 LSTVTLT--QOKLAGTALSFLPLRXSPGPIGGANRDISILQCHGDCDPLVPLMFG 160
118 VLTAFARRAQLPLGVALSTYAP--TFDDALDERHRIRIPLVHLHSGODDVVDPALG 174
161 SLTVEKLTLYNPANVTFKTEGMMHSSCOQEMMDVKOFIDK 204
175 RAADALQ--AQGYEVGMHDYR-MGHEVLSLEIHDIGAMLRKL 215

RESULT 7

JU0277
carboxylesterase (EC 3.1.1.1) - Pseudomonas fluorescens
N:Alternate names: esterase II
C:Species: Pseudomonas fluorescens
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Mar-2000
C:Accession: JU0277
R:Hong, K.H.; Jang, W.H.; Jang, K.D.; Yoo, O.J.
Agric. Biol. Chem. 55, 2839-2845, 1991
A:Title: Characterization of Pseudomonas fluorescens carboxylesterase: cloning and ex
A:Reference number: JU0277; M0ID:92134742; PMID:1368750
A:Accession: JU0277
A:Molecule type: DNA
A:Residues: 1-218 <HON>
A:Cross-references: GB:S79600; NID:g244500; PIDN:AAC60403.1; PID:g244501
C:Genetics:
A:Gene: estB
C:Keywords: carboxylic ester hydrolase
F:114/Active site: Ser #status predicted

Query Match 22.9%; Score 245; DB 2; Length 218;
Best Local Similarity 33.0%; Pred. No. 1.9e-15;
Matches 70; Conservative 30; Mismatches 80; Indels 32; Gaps 6;

11 PAIVPAARKATAAVIFLHGLG-----DTGPRVPVTINMNV 46
4 PULIQPAKPADACIYIMHGLGADRDYDFKPVAEALQESLITTRFVLPQAPTRVYTINGYE 63
47 MSPWEDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGALS 106
64 MSPWDIKAMSPARSISLEBELVSAMKMYDILAEQKRTCIDASRIEFLAGFSOGGAVVPT 123
107 A-LTQOKLAGTALSFLPLRXSF--PGGPIGGANRDISILQCHGDCDPLVPLMFGSLTV 164
124 APLNMWGPGLGVYALSTYAP--TFDELELSAQQRIPALCLHGOYDVVONAMGRSAF 180
165 EKLTLYNPANVTFKTEGMMHSSCOQEMMDV 196
181 EHLKS--RGVYTWQEXR-MGHEVLPQELIHI 209

RESULT 8

JQ0885
esterase A (EC 3.1.1.-) - Pseudomonas fluorescens
C:Species: Pseudomonas fluorescens
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Mar-1996
C:Accession: JQ0885
R:Yu, F.
submitted to JIPID, March 1991
A:Reference number: JQ0885
A:Accession: JQ0885
A:Molecule type: DNA
A:Residues: 1-218 <YUF>
A:Experimental source: strain IF03081
C:Genetics:
A:Gene: estA
C:Keywords: carboxylic ester hydrolase

Query Match 22.8%; Score 244; DB 2; Length 218;
Best Local Similarity 32.0%; Pred. No. 2.4e-15;
Matches 70; Conservative 31; Mismatches 88; Indels 30; Gaps 5;

11 PAIVPAARKATAAVIFLHGLG-----DTGPRVPVTINMNV 46
4 PULIQPAKPADACIYIMHGLGADRDYDFKPVAEALQETILSTRFVLPQAPTRVYTINGYE 63
47 MSPWEDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGALS 106
64 MSPWDIKAMSPARSISLEBELVSAMKMYDILAEQKRTCIDASRIEFLAGFSOGGAVVPT 123
107 ALTT--QOKLAGTALSFLPLRXSPGPIGGANRDISILQCHGDCDPLVPLMFSLVE 165
124 AFKWEGLGVYALSTYAPTFDNDLQ--LSASQQRIPFLCLHGOYDEVONAMGRSAF 181

Tue Jan 21 10:18:28 2003

us-09-988-982-1.rpr

Page 6

QY 150 DCDPLVPIMGSLTVEKLTLVNPNANVFYEKTIEGMHSSCQQ 191
 : | : | : | : | :
Db 162 -----HPFHVPYLFEKRRLHCSCSE 181

Search completed: January 19, 2003, 03:24:47
Job time : 79 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 19, 2003, 02:36:55; Search time 78 Seconds
(without alignments)
110.604 Million cell updates/sec

Title: US-09-988-982-1

Perfect score: 1070
Sequence: 1 MCGNNMSTPLPAIVPARKA.....COQEMMDVQFIDKLPPID 208

Scoring table: BLOSUM62
Gapop 10.0, Gapect 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	245	22.9	218	1	EST2_PSEFL
2	244	22.8	218	1	EST1_PSEFL
3	126	11.8	241	1	YE88_SCHPO
4	90.5	8.5	232	1	YFPH_ECOLI
5	89.5	8.4	219	1	CUT2_MYCTU
6	88.5	8.3	215	1	Y744_RICPR
7	84	7.9	252	1	CLCD_RHOOP
8	84	7.9	705	1	CANX_CHICK
9	83	7.8	501	1	Y890_THEMA
10	82	7.7	655	1	RRAL_CABEL
11	81.5	7.6	320	1	HEM3_SYNY3
12	81.5	7.6	358	1	LIP_PSEFL
13	80.5	7.5	271	1	EST2_PSEFL
14	80	7.5	370	1	ACOC_PSEPU
15	79.5	7.4	608	1	BDD_PSEAE
16	79	7.4	217	1	CUT1_MYCTU
17	79	7.4	247	1	CUT3_MYCTU
18	79	7.4	400	1	YIEL_ECOLI
19	78.5	7.3	275	1	PRXC_STRLI
20	78.5	7.3	284	1	BCHO_RHOCA
21	78.5	7.3	399	1	DKR_AMASP
22	78.5	7.3	749	1	PA24_HORSE
23	77.5	7.2	364	1	LIP_BURCE
24	77.5	7.2	969	1	MSU1_YEAST
25	77	7.2	247	1	YFBB_HAEIN
26	77	7.2	580	1	PROA_XANCP
27	76.5	7.1	245	1	HIS4_YERPE
28	76.5	7.1	449	1	HTRA_BACSU
29	76	7.1	263	1	PI7A_ORYSA
30	76	7.1	319	1	ABE_ECOLI
31	76	7.1	417	1	PGK_CANNA
32	76	7.1	429	1	HISX_METJA
33	76	7.1	954	1	BTRL_YEAST

34	76	7.1	1162	1	LEPR_RAT	O62959 rattus norv
35	75.5	7.1	364	1	LIP_PSESS	P25275 pseudomonas
36	75.5	7.1	754	1	MBPL_KLUTA	P39679 kluyveromyc
37	75.5	7.1	837	1	XINZ_CLOTH	P10478 clostridium
38	75.5	7.1	1081	1	CARB_RALSO	O8x283 ralstonia s
39	75	7.0	230	1	CUT1_PUSSC	O99174 fusarium so
40	75	7.0	414	1	PHAI_PSELE	P52090 pseudomonas
41	75	7.0	785	1	MUS2_BACSU	P94545 bacillus su
42	75	7.0	381	1	PCGV_BOVIN	P81282 bos taurus
43	74.5	7.0	235	1	BTRL_RAT	P55007 rattus norv
44	74.5	7.0	1275	1	COBN_PSEDE	P29929 pseudomonas
45	74	6.9	428	1	YEB3_SCHPO	O14249 schizosacch

ALIGNMENTS

RESULT 1
EST2_PSEFL
ID EST2_PSEFL STANDARD: PRT: 218 AA.
AC Q5347;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Carboxylesterase 2 (EC 3.1.1.1) (Esterase II).
GN ESTB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92134742; PubMed=1368750.
RA Hong K.H., Jang W.H., Choi K.D., Yoo O.J.;
RT "Characterization of Pseudomonas fluorescens carboxylesterase:
RT cloning and expression of the esterase gene in Escherichia coli.";
RL Agric. Biol. Chem. 55:2839-2845(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=98104086; PubMed=9438866.
RA Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Choe S., Yoo O.J.,
RA Suh S.W.;
RT "Crystal structure of carboxylesterase from Pseudomonas fluorescens,
RT an alpha/beta hydrolase with broad substrate specificity.";
RL Structure 5:1571-1584(1997).
CC - FUNCTION: HYDROLYSE CARBOXYLIC ESTER BONDS WITH RELATIVELY BROAD
CC SUBSTRATE SPECIFICITY.
CC - CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC - SUBUNIT: HOMODIMER.
CC
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CC
CC EMBL: S79600; AAC60403.1; -
CC DR PDB: LAUD; 04-MAR-98.
CC DR PDB: LAUD; 04-MAR-98.
CC DR InterPro: IPR003140; PLP_Gesterase.
CC DR InterPro: IPR003140; Ser_estrs_site.
CC DR Pfam: PF02230; abhydrolase_2; 1.
CC KW Hydrolase; Serine esterase; 3D-structure.
CC FT ACT_SITE 114 114 CHARGE RELAY SYSTEM.
CC FT ACT_SITE 168 168 CHARGE RELAY SYSTEM.
CC FT ACT_SITE 199 199 CHARGE RELAY SYSTEM.
CC SQ SEQUENCE 218 AA; 23880 MW; 6FID4537410E4CB4 CRC64;
Query Match 22.9%; Score 245; DB 1; Length 218;
Best Local Similarity 33.0%; Pred. No. 1,9e-15;

	Query Match	22.88;	Score 244;	DB 1;	Length 218;
	Best Local Similarity	32.08;	Pred. No. 2.4e-15;		
	Matches 70;	Conservative 31;	Mismatches 88;	Indels 30;	Gaps 5;
QY	11 PAIIPAARKATAAAYIFLGLG-----DTGVPRPVTLNNMVA	46			
	: :				
Dd	4 PLIIQPAKPADACIWIHLGCADRYDFLPVAAEQETLLSTRFVLPPQAFTPTVIITNGYE	63			
	: : : : : : : : : : : : : :				
QY	47 MPSEWEDIIIGSPDSEDSEGIRKQAENIKALIDDEVKNKGIIPSNRIILGGFSOGALSLEYT	106			
	: : : : : : : : : : : :				
Dd	64 MPSWDYDIKAMSPARSISILEELETSAKTFTVDLIETQRFGIDITSRLFLAGFSQGAVYEHY	123			
	: : : : : : : : : : : :				
QY	107 ALTI-QOKLAGVTALSFLLPLRKXSFPGPGIGCANNDISILOCHDCDPVLPMRGSLTVE	165			

```

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CC CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z98763; CAB11492.1; -.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_cstrs_site.
DR Pfam; PF02230; adhydro1ase_2; 1.
DR Hypothetical protein.
KW
SQ SEQUENCE 241 AA; 27341 MW; BEF6C2D1B7DBFE21 CRC64;

Query Match 11.8%; Score 126; DB 1; Length 241;
Best Local Similarity 20.7%; Pred. No. 0.0002;
Matches 46; Conservative 35; Mismatches 65; Indels 76; Gaps 7;
y 4 NNNKSTPLPA-----IVPAARKATAAIVFLHGLGDT-----GPV 36

```


CC Thermotogaceae: Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *Thermotoga maritima*.";
 RL Nature 399:323-329(1999).
 CC -1- CORFACTOR: Zinc (Probable).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 (By similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE001754; MADS5971.1; -
 CC TIGR: TM0890; -
 DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR000130; Zn_MTPeptidase.
 DR Pfam: PF00595; PDZ; 1.
 DR SMART: SM00226; PDZ; 1.
 DR PROSITE: PS50106; PDZ; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR Hypothetical protein: Hydrolase; Metalloprotease; Zinc; Transmembrane;
 KW Inner membrane; Complete proteome.
 FT METAL 17 17 ZINC (CATALYTIC) (POTENTIAL).
 FT ACT_SITE 18 18 POTENTIAL.
 FT METAL 21 21 ZINC (CATALYTIC) (POTENTIAL).
 FT TRANSMEM 93 115 POTENTIAL.
 FT TRANSMEM 401 420 POTENTIAL.
 FT TRANSMEM 427 449 POTENTIAL.
 FT TRANSMEM 474 496 POTENTIAL.
 FT DOMAIN 96 180 PDZ.
 SO SEQUENCE 501 AA; 55875 MW; CE3E58117DC2A9A CRC64;
 Query Match 7.8%; Score 83; DB 1; Length 501;
 Best Local Similarity 25.8%; Pred. No. 4.3;
 Matches 31; Conservative 24; Mismatches 43; Indels 22; Gaps 7;
 OY 38 PVTLMNVMVPSWFDIIGSPDSQDESGIKQA-----AENIK-----ALIDQVKNKIPS 88
 DB 113 PVTLMNVMVPSWFDIIGSPDSQDESGIKQA-----AENIK-----ALIDQVKNKIPS 169
 OY 89 NRITLGGSGGALSITLTATTOOKLAGVTALSFLLPKRSPFOGPI--CGANRDISIQ 146
 DB 170 ELVTI--RNKGKSL--RLTPMY--PETYETVLESADGIPSGKLYSVNGNRDTSYK 221
 RESULT 10
 RFAL CAEEL
 ID RFAL CAEEL STANDARD; PRT; 655 AA.
 AC 019537;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Probable replication factor A 73 kDa subunit (RP-A) (RF-A)
 DE (Replication factor-A protein 1).
 FI 181.5.
 GN Caenorhabditis elegans.

CC Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Kirsten J.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO SINGLE-STRANDED SEQUENCES (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: TO OTHER SPECIES RFAL/RFAL.
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 CC -----
 CC EMBL: U41535; AAB63407.1; -
 DR HSSP: P27694; LJC.
 DR WormPep: F18A1.5; CE04405.
 DR InterPro: IPR004591; Rpal.
 DR InterPro: IPR004365; RNA_antl.
 DR Pfam: PF01336; RNA_antl; 2.
 DR TIGRFAMs: TIGR00617; rpal; 1.
 KW DNA replication; DNA-binding; Zinc-finger; Nuclear protein.
 FT ZN_FING 518 539
 SO SEQUENCE 655 AA; 73202 MW; 44E41E7B16E2FB42 CRC64;
 Query Match 7.7%; Score 82; DB 1; Length 655;
 Best Local Similarity 26.9%; Pred. No. 7.4;
 Matches 42; Conservative 19; Mismatches 57; Indels 38; Gaps 8;
 OY 63 DESG-----IKQAMENIKALIDQVKNKIPSNRII-----LGSFGGALSITLTATTOOK 113
 DB 387 DESGALVRLTLMGDEATLALDDVYOKVIARFVGFPGFSLGTGSA--PFIISVPE 444
 OY 114 LAGVAL-----SFLLPKRXSPFOGPIGKAN--RDISILQCHDCDPLVPMFGS---- 161
 DB 445 IAGVELDWTANAKPTTEVKMMSQAGSNEAPRTTAGLD-----EMQGRKSDK 495
 OY 162 --LFEVKIKTLVNPANVTFTYEGMMSQCOEEM 194
 DB 496 GDYATVKAMITRVNPTNA---LYRGCASEGCGKTLV 528
 RESULT 11
 HEM3-SYNY3
 ID HEM3-SYNY3 STANDARD; PRT; 320 AA.
 AC P73660;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Porphobilinogen deaminase (EC 4.3.1.8) (PBG) (Hydroxymethylblane
 synthase) (HMB) (Pre-uroporphyrinogen synthase).
 GN HEMC OR SLR187.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA MiyaJima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Natsu K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).
 CC -1- FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PB6 INTO THE
 CC HYDROXYMETHYLBILANE PREDOPORPHIRINOGEN IN SEVERAL DISCRETE STEPS.
 CC -1- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O =
 CC hydroxymethylbilane + 4 NH(3).
 CC -1- COFACTOR: COVALENTLY BINDS A DIPHYROMETHANE COFACTOR TO WHICH
 CC THE PORPHOBILINOGEN SUBUNITS ARE ADDED.
 CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
 CC Involved in chlorophyll biosynthesis.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HMBS FAMILY.
 CC -----
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 CC -----
 DR EMBL; D90908; BAA17705.1; -.
 DR HSP; P06983; IPDA.
 DR InterPro; IPR000860; Porphobil_deam.
 DR Pfam; PF01379; Porphobil_deam; 1.
 DR PRINTS; PR00151; PORPHBDNMASE.
 DR ProDom; PD002745; Porphobil_deam; 1.
 DR TIGRFAMs; TIGR00212; hemc; 1.
 DR PROSITE; PS00533; PORPHOBILINOGEN_DEAM; 1.
 DR Porphyrin biosynthesis; Chlorophyll biosynthesis; Lyase;
 DR Complete proteome.
 FT BINDING 249 249 PYRROMETHANE COFACTOR (BY SIMILARITY).
 SO SEQUENCE 320 AA; 34894 MW; 6A3C9CAF81CA183 CRC64;

Query Match 7.6%; Score 81.5; DB 1; Length 320;
 Best Local Similarity 21.2%; Pred. No. 3.4;
 Matches 48; Conservative 40; Mismatches 81; Indels 57; Gaps 8;

QY 6 MSTPLAIVPARKATAVIFLHGLGPTGVPRTYLMNVAMPSPFDIGLSPDSODES 65
 Db 3 VSTSPVYRISRSKSQLAVOTYVOE-----ELQKHPFPRQDVE 43
 QY 66 GIKQAENI-----KALIDQEVKNGIPNRILIGSGGALSTYALTQCKLA 115
 Db 44 TMEQGDILDLVALAKIGDKGLFTQELJEDGMLKRTDLAVHS---LKDLPNLNLAGMLG 100
 QY 116 GVT-----ALSFLLPLR-----XSPFGPGGAN--RDISILQCHDCDPLVPLMGSL 162
 Db 101 CVTRKVPADALVLANRQCKDLASLPEGAIVGTSSLRRLAQLRYH-----FPHL 150
 QY 163 TVERKLTLPN--ANVTFKTEGMMHSSCOEEMDVAKQFIDKLLP 206
 Db 151 TFKVGRNVNTRLAKLDSNEYDAITLLAAGLERLDMANRIDOLIP 196

RESULT 12
 LIP_PSEGL STANDARD; PRT; 358 AA.
 AC 005489;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIPA.
 OS Pseudomonas glumae, and
 OS Chromobacterium viscosum.
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
 OC Burkholderia.
 OX NCBI_TaxID=337, 42739;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 40-61, AND MUTAGENESIS.
 RC SPECIES-P. glumae; STRAIN-PGI / CBS 322.89;
 RX MEDLINE=93119130; PubMed=1476423;
 RA Frenken L.G.J., Egmund M.R., Batenburg A.M., Bos J.W., Visser C.,

RA Verrips C.T.;
 RT "Cloning of the Pseudomonas glumae lipase gene and determination of
 RT the active site residues."; Appl. Environ. Microbiol. 58:3787-3791(1992).
 RL [2]
 RN SEQUENCE OF 40-54, AND CHARACTERIZATION.
 RP SPECIES-C. viscosum;
 RC MEDLINE=95305600; PubMed=7786905;
 RX Taipa M.A., Liebeton K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
 RT Lipase from Chromobacterium viscosum: biochemical characterization
 RT indicating homology to the lipase from Pseudomonas glumae."; Biochim. Biophys. Acta 1256:396-402(1995).
 RL [3]
 RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RP SPECIES-P. glumae; PubMed=8405390;
 RC MEDLINE=94009622; PubMed=8405390;
 RX Noble M.E.M., Cleasby A., Johnson L.N., Egmund M.R., Frenken L.G.J.;
 RT "The crystal structure of triacylglycerol lipase from Pseudomonas
 RT glumae reveals a partially redundant catalytic aspartate."; FEBS Lett. 331:123-128(1993).
 RL [4]
 RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RP SPECIES-C. viscosum; STRAIN-ATCC 6918;
 RX MEDLINE=96275656; PubMed=8683577;
 RA Lang D., Hofmann B., Haalick L., Hecht H.-J., Spener F., Schmid R.D.,
 RA Schomburg D.;
 RT "Crystal structure of a bacterial lipase from Chromobacterium
 RT viscosum ATCC 6918 refined at 1.6-A resolution."; J. Mol. Biol. 259:704-717(1996).
 RL [5]
 CC -1- FUNCTION: HYDROLYSIS OF TRIGLUCERIDES.
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
 CC LIPASE FAMILY.
 CC -----
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X70354; CAA49812.1; -.
 DR EMBL; A16323; CAA01279.1; -.
 DR EMBL; A32021; CAA02073.1; -.
 DR PIR; A48952; A48952.
 DR PIR; S37291; S37291.
 DR PDB; 1TAH; 31-MAY-94.
 DR InterPro; IPR000073; Abhydrolase.
 DR InterPro; IPR000734; Lipase.
 DR InterPro; IPR000379; Serestsr_site.
 DR Pfam; PR00561; abhydrolase; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolyase; Lipid degradation; Signal; Calcium; 3D-structure.
 FT SIGNAL 1 39
 FT CHAIN 40 358
 FT ACT_SITE 126 126
 FT ACT_SITE 302 302
 FT ACT_SITE 324 324
 FT ACT_SITE 324 324
 FT DISULFID 229 308
 FT MUTAGEN 54 54
 FT MUTAGEN 126 126
 FT MUTAGEN 160 160
 FT MUTAGEN 160 160
 FT MUTAGEN 160 160
 FT MUTAGEN 280 280
 FT MUTAGEN 280 280
 FT MUTAGEN 302 302
 FT MUTAGEN 302 302
 H->A: NO LOSS OF ACTIVITY.
 S->A: COMPLETE LOSS OF ACTIVITY.
 D->E: NO LOSS OF ACTIVITY.
 D->A: NO LOSS OF ACTIVITY.
 D->E: NO LOSS OF ACTIVITY.
 D->A: COMPLETE LOSS OF ACTIVITY.
 D->E: NO LOSS OF ACTIVITY.
 D->A: 75% LOSS OF ACTIVITY.

FT MUTAGEN 324 324 H->A: COMPLETE LOSS OF ACTIVITY.
 FT CONFLICT 40 40 A -> W (IN REF. 2).
 SQ SEQUENCE 358 AA: 36928 MW: FE7B5D7A22EC6B4B CRC64:

Query Match
 Best Local Similarity 27.0%; Pred. No. 3.9;
 Matches 34; Conservative 13; Mismatches 52; Indels 27; Gaps 5;

QY 11 PAIVPAKAKATA-AVIFLHGLDGPVAPVPLNNVAMPSEFDLIGLSPDSQ----- 61
 DB 35 PAIVAADVYAAATVPVILVHGLAGTDFKPAV-----VDVY---GIQSDLQSHGAKVY 84
 QY 62 -----EDESGLKQAEENIKALIDQEVNKGIPSNRIILIGFSGGALSLYATLTTOOKL 114
 DB 85 VANLSFGSDGPGNGRGEOLLAVVVO-VLAATGATKRVNLIGHSGGINSRYVAAPOLV 143
 QY 115 AGVTAL 120
 DB 144 ASVTTI 149

RESULT 13
 ESTE_PSEFL STANDARD: PRT: 271 AA.

ID AC P22862;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Arylesterase (EC 3.1.1.2) (Aryl-ester hydrolase).
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SIK WI;
 RC MEDLINE=95219101; PubMed=7704276;
 RA Pelletier I., Altenbucher J.;
 RT "A bacterial esterase is homologous with non-haem haloperoxidases and displays brominating activity.";
 RT Microbiology 141:459-468(1995).
 RN [2]
 RP PRELIMINARY SEQUENCE FROM N.A., AND SEQUENCE OF 1-17.

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 CC EMBL: U12537; AAB60168.1; -
 CC EMBL: D12484; BAA02052.1; ALT_FRAME.
 CC FTR: J00606; J00606.
 CC DR HSSP: O31158; IAS8.
 CC DR InterPro: IPR000073; Abhydrolase.
 CC DR InterPro: IPR000379; Ser_estr_site.
 CC DR Pfam: PF00561; abhydrolase; 1.
 CC KM Hydrolase.
 CC FT INTL_MET 0 0 BY SIMILARITY.
 CC FT ACT_SITE 94 94

FT ACT_SITE 222 222 BY SIMILARITY.
 FT ACT_SITE 251 251 BY SIMILARITY.
 SQ SEQUENCE 271 AA: 29961 MW: 1ADA219AD8130123 CRC64;

Query Match
 Best Local Similarity 19.5%; Pred. No. 3.5;
 Matches 41; Conservative 23; Mismatches 57; Indels 89; Gaps 8;

QY 71 AENIKALIDQEVNKGIPSNRIILIGFSGGALSLYATLTTOOKLAVTALSFLLPL-- 126
 DB 73 ADDIAQLIEH-----DLKEVTLVGFSMGGDVARYIARRGSAKVAGVLGAVTPLFGQ 127
 QY 127 RXSEPGQ-----PIGAGR----- 140
 DB 128 KPDYQGVPLDVFAFKTELLKDRAGFISDPNAPFYGINKGQVVSQGVOTQIALLAS 187
 QY 141 -----DISTLQCHGDDPLVPL-MGSLTVERKTLVNPANY 176
 DB 188 LKATVDCVTAFAETDFRPMKIDVPLVLVHGDDQIVPEFTTGKVAELIK-----GA 241
 QY 177 TFKTYEGMMH-----SSCOEMMDVKQFIDK 202
 DB 242 ELKVTYKAPRPFATVTHAQQLMEDLAFLEKR 271

RESULT 14
 ACOC_PSEPU STANDARD: PRT: 370 AA.

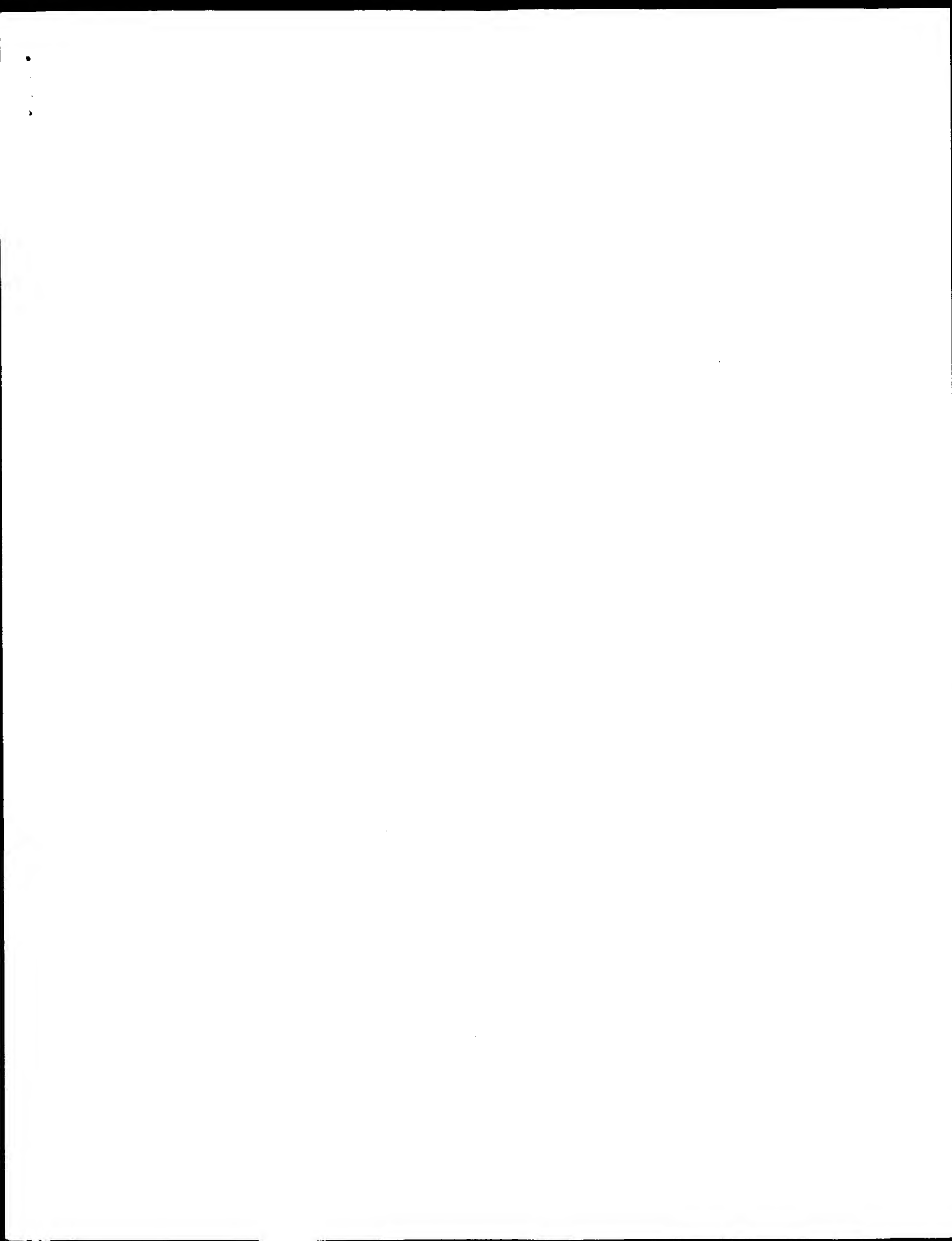
ID ACOC_PSEPU
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dihydrolipoamide acetyltransferase component of acetyl CoA cleaving system (EC 2.3.1.12) (Acetyl CoA dehydrogenase E2 component).
 DE ACOC.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PBG2;
 RC MEDLINE=95113288; PubMed=7813883;
 RA Huang M., Oppermann F.B., Steinbuechel A.;
 RT "Molecular characterization of the Pseudomonas putida 2,3-butanediol catabolic pathway.";
 RT FEBS Microbiol. Lett. 124:141-150(1994).
 RL FEMS Microbiol. Lett. 124:141-150(1994).
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-acetyl dihydrolipoamide.
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
 CC -1- PATHWAY: Acetyl CoA catabolism.
 CC -1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.

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 CC EMBL: L35343; AAB58981.1; -
 CC DR HSSP: P10515; IFYC.
 CC DR InterPro: IPR003089; AB_hydrolase.
 CC DR InterPro: IPR000073; Abhydrolase.
 CC DR InterPro: IPR000089; Biotin_lipoyl.
 CC DR InterPro: IPR003016; Lipoyl.
 CC DR InterPro: IPR000379; Ser_estr_site.
 CC DR Pfam: PF00364; biotin_lipoyl; 1.
 CC DR Pfam: PF00561; abhydrolase; 1.
 CC DR PRINTS: PR00111; ABHYDROLASE.
 CC DR PROSITE: PS00189; LIPOYL; 1.

KM Transferase; Acyltransferase; Lipoyl.
 FT DOMAIN 1 78 LIPOYL BINDING.
 FT BINDING 45 45 LIPOYL (BY SIMILARITY).
 SQ SEQUENCE 370 AA; 39638 MW; F3DF2A23B14983B9F CRC64;
 Query Match 7.5%; Score 80; DB 1; Length 370;
 Best Local Similarity 20.9%; Pred. No. 5.6;
 Matches 41; Conservative 35; Mismatches 68; Indels 52; Gaps 8;
 OY 15 PAARATATA-----VFHGLGDTGPRPTLMMNVAAMPSPWFIITLS- 57
 DB 111 PAPQAEVGGALLKMFELGGGCTPLVAVHFG--GDIINMKNFN-HPPLAERRVIALDL 167
 OY 58 PDSEDESGIK-----QAENIKALIDQEVKNGIPSNRIILGFSOGGALSLYTALTTOQ 112
 DB 168 PCHGESAKALRGDLDDELSETVLALDH-----LDIAKAKHLAGSHMGAVSLNVAAGLAPQ 222
 OY 113 KLAGVTALSLF---LPLKXSPQGPFGGANDISILQCHGDDPLVPLMREGSLTVERKLT 169
 DB 223 RVASLSLTSASGLGEALNGOYLQGFVAANFN-----ALKPQWVOL 263
 OY 170 LVNPANVTFTYEGMM 185
 DB 264 FADPALVTRQMLEDM 279
 RESULT 15
 EDD_PSEAE STANDARD; PRT; 608 AA.
 ID EDD_PSEAE STANDARD; PRT; 608 AA.
 AC P31961; 09HZ45;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phosphoglucuronate dehydratase (EC 4.2.1.12) (6-phosphogluconate dehydratase)
 GN EDD OR PA3194.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=94321343; PubMed=8045900;
 RA Temple L.M., Sage A., Christie G.E., Phipps P.V. Jr.;
 RA "Two genes for carbohydrate catabolism are divergently transcribed from a region of DNA containing the hexC locus in Pseudomonas aeruginosa PAO1.";
 RT J. Bacteriol. 176:4700-4709(1994).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P., Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
 RT Nature 406:959-964(2000).
 RL Nature 406:959-964(2000).
 CC -1- CATALYTIC ACTIVITY: 6-phospho-D-gluconate = 2-dehydro-3-deoxy-6-phospho-D-gluconate + H(2)O
 CC -1- PATHWAY: KEY ENZYME IN THE ENTERO-DUODOROFF PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
 CC -----
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 CC -----
 DR EMBL: M74256; AAA03487.1; -.
 DR EMBL: AE004743; AAC06582.1; -.
 DR InterPro: IPR004786; Edd.
 DR InterPro: IPR000581; ILVD_EDD_family.
 DR Pfam: PF00920; ILVD_EDD_1.
 DR ProDom: PD002691; ILVD_EDD_family; 1.
 DR TIGRFAMS: TIGR01196; edd; 1.
 DR PROSITE: PS00886; ILVD_EDD_1; 1.
 DR PROSITE: PS00887; ILVD_EDD_2; 1.
 DR Lyase; Complete proteome.
 FT CONFLICT 84 88 FERFP -> VRAPFR (IN REF. 1).
 FT CONFLICT 93 104 QALHEIGSVGQF -> PGACTRSVRSASV (IN REF. 1).
 FT CONFLICT 163 167 TGSRL -> SAS (IN REF. 1).
 FT CONFLICT 178 178 A -> G (IN REF. 1).
 FT CONFLICT 232 232 L -> VR (IN REF. 1).
 FT CONFLICT 258 258 T -> S (IN REF. 1).
 SQ SEQUENCE 608 AA; 65182 MW; 1C2A415B32B95911 CRC64;
 Query Match 7.4%; Score 79.5; DB 1; Length 608;
 Best Local Similarity 24.8%; Pred. No. 11;
 Matches 38; Conservative 26; Mismatches 62; Indels 27; Gaps 7;
 OY 28 HGLGDTGPRPTLNM-----NVAMPSPF-DIIGLSPDSQDESGIKQAENIKALIDQEV 82
 DB 47 HGYAAGGESDKQTLRLMNQANVAIVASYNMLSAHQPFERFRELKQALHEIGSV--GGF 104
 OY 83 KNGIPSNRIILGFSOGGALSLYTALTTOQKLAGVATLSFLPLKXSPQGPFGGANDRI 142
 DB 105 AGGVPA---MCDGVTOGEP-GMELSLASRDVIAMSTAL-----SHNMF 145
 OY 143 SILQCHGDDPLVP-LMFGSLTVERKLTIVNPA 174
 DB 146 DAALCLGVCCKIVPGLLISLRGHLPTVFPVA 178

Search completed: January 19, 2003, 03:21:31
 Job time : 100 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2003, 03:14:05 ; Search time 112 Seconds
(without alignments)
382.659 Million cell updates/sec

Title: US-09-988-982-1

Perfect score: 1070
Sequence: 1 MCGNNMSTPLPAIVAPARRA.....COQEMNDVKQFIDKLPPID 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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1: SPTRMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriophage:*
18: sp_bacteriophage:*
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43: sp_bacteriophage:*
44: sp_bacteriophage:*
45: sp_bacteriophage:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1034	96.6	230	4	075608
2	968	90.5	230	6	077821
3	968	90.5	230	11	P97823
4	958	89.5	230	11	P70470
5	949	88.7	214	4	Q9UQF9
6	935	87.4	219	6	077820
7	723	67.6	231	11	Q9QYU8
8	717	67.0	231	11	Q9QYU8
9	713	66.6	231	11	Q9QYU8
10	672	62.8	231	4	Q9UQF9
11	499	46.6	104	4	Q43202
12	490	45.8	216	5	Q917R0
13	422.5	39.5	223	5	Q21224
14	406.5	38.0	227	5	Q9UQF2
15	406.5	38.0	229	5	Q18501
16	397	37.1	245	3	Q9HJ55

17	318.5	29.8	224	3	042881	042881 schizosacch
18	306	28.6	227	3	Q12354	Q12354 saccharomyc
19	273.5	25.6	224	16	Q9PCY0	Q9PCY0 xyloella fas
20	265	24.8	235	5	Q9YGV9	Q9YGV9 drosophila
21	248	23.2	215	16	Q9HXE7	Q9HXE7 pseudomonas
22	240.5	22.5	471	10	Q4635	Q4635 arabidopsis
23	238	22.2	239	11	Q8R065	Q8R065 mus musculu
24	227.5	21.3	237	4	Q96AV0	Q96AV0 homo sapien
25	209.5	19.6	257	10	Q94E46	Q94E46 oryza sativ
26	205.5	19.2	255	10	Q91W14	Q91W14 arabidopsis
27	172	16.1	195	10	Q9SSS4	Q9SSS4 arabidopsis
28	163.5	15.3	204	16	P73192	P73192 synecocyst
29	145.5	13.6	207	2	Q53415	Q53415 spirulina p
30	134	12.5	214	16	Q8YSH2	Q8YSH2 anabaena sp
31	128.5	12.0	243	16	Q9Z8R7	Q9Z8R7 chlamydia p
32	124	11.6	161	10	Q9SSS3	Q9SSS3 arabidopsis
33	120.5	11.3	200	10	Q9FTU7	Q9FTU7 oryza sativ
34	120.5	11.3	305	5	Q9XVAT	Q9XVAT caenorhabdi
35	119.5	11.2	126	10	Q9FZP5	Q9FZP5 arabidopsis
36	116	10.8	302	2	Q49658	Q49658 mycobacteri
37	116	10.8	304	16	Q9CCU5	Q9CCU5 mycobacteri
38	115	10.7	304	16	P69903	P69903 mycobacteri
39	108	10.1	239	16	Q9PKQ2	Q9PKQ2 chlamydia m
40	108	10.1	319	16	Q8Y518	Q8Y518 listeria mo
41	105.5	9.9	204	16	Q9KAW2	Q9KAW2 bacillus ha
42	105.5	9.9	243	16	Q92W16	Q92W16 rhizobium m
43	100.5	9.4	344	16	Q8XYI6	Q8XYI6 ralsstonia s
44	100	9.3	300	16	Q8XW2	Q8XW2 ralsstonia s
45	100	9.3	335	5	Q9XVB2	Q9XVB2 caenorhabdi

ALIGNMENTS

```

RESULT 1
ID 075608 PRELIMINARY: PRT: 230 AA.
AC 075608:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Lysophospholipase (Acyl-protein thioesterase-1) (lysophospholipase
DE I).
DE LPI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Hu G.;
RA Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shen Y., Guan Z., Gu J., Ye M., Zhou J., Zhang Q., Xu S., He K.,
RA Chen S., Mao M., Chen Z.;
RA "Human lysophospholipase gene.";
RA Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RX Pubmed=11080636;
RN [3]
RP SEQUENCE FROM N.A.
RA Devdajev Y., Dauter Z., Kuznetsov S.R., Jones T.L., Derewenda Z.S.;
RA "Crystal structure of the Human Acyl Protein Thioesterase I from a
RA single X-Ray data set to 1.5 A.";
RA Structure 8:1137-1146(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA TISSUE-BONE MARROW;
RA Strusberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA TISSUE-EYE;

```

RA Strausberg R.;
 RL Submitted (May-2001) to the EMBL/Genbank/DBDJ databases.
 DR EMBL: AF081281; AAC31610.1; -
 DR EMBL: AF077198; AAD26993.1; -
 DR EMBL: AF291053; AAG10063.1; -
 DR EMBL: BC010397; AAH10397.1; -
 DR EMBL: BC008652; AAH08652.1; -
 DR HSSP: 053547; IAUO.
 DR PMAA-2DPAGE; 075608; -
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 SQ SEQUENCE 230 AA; 24669 MW; 90C0522F765FIAC6 CRC64;

Query Match 96.6%; Score 1034; DB 4; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.2e-92;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPARAKATAVIFLHGLGDTG-----PVRP 38
 DB 1 MCGNNMSTPLPAIVPARAKATAVIFLHGLGDTGMAEAFAGIRSHIKYICPHAPVP 60
 QY 39 VTLNMANVAMPSEFDTIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 DB 61 VTLNMANVAMPSEFDTIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGLSLVLTALTTQOKLAGVATLFLPRKSPGPIGGANDISILQCHGCDPLVPLM 158
 DB 121 GGLSLVLTALTTQOKLAGVATLFLPRKSPGPIGGANDISILQCHGCDPLVPLM 180
 QY 159 FGSILTEKLTIVNPANVTERTYEGMHHSSCOQEMMDVKQFTDKLLPID 208
 DB 181 FGSILTEKLTIVNPANVTERTYEGMHHSSCOQEMMDVKQFTDKLLPID 230

RESULT 2
 077821 PRELIMINARY; PRT; 230 AA.
 AC 077821;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Calcium-independent phospholipase A2 isoform 2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=98308497; PubMed=9644627;
 RA Porcilia D., Crew M.D., Grant D., Serrero G., Bates L.M., Dal G.,
 RA Sasser M., Cheng J., Buonanno A.;
 RT "CDNA cloning and expression of a novel family of enzymes with
 RT calcium-independent phospholipase A2 and lysophospholipase
 RT activities.";
 RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
 DR EMBL: U97148; AAC63432.1; -
 DR HSSP: 053547; IAUO.
 DR InterPro: IPR002106; AATRNA_ligaset1.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 DR PROSITE: PS00339; AA TRNA LIGASE II 2; UNKNOWN 1.
 SQ SEQUENCE 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;

Query Match 90.5%; Score 968; DB 6; Length 230;
 Best Local Similarity 81.7%; Pred. No. 3.1e-86;
 Matches 188; Conservative 8; Mismatches 12; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPARAKATAVIFLHGLGDTG-----PVRP 38
 DB 1 MCGNNMSTPLPAIVPARAKATAVIFLHGLGDTGMAEAFAGIRSHIKYICPHAPVP 60

QY 39 VTLNMANVAMPSEFDTIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 DB 61 VTLNMANVAMPSEFDTIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGLSLVLTALTTQOKLAGVATLFLPRKSPGPIGGANDISILQCHGCDPLVPLM 158
 DB 121 GGLSLVLTALTTQOKLAGVATLFLPRKSPGPIGGANDISILQCHGCDPLVPLM 180
 QY 159 FGSILTEKLTIVNPANVTERTYEGMHHSSCOQEMMDVKQFTDKLLPID 208
 DB 181 FGSILTEKLTIVNPANVTERTYEGMHHSSCOQEMMDVKQFTDKLLPID 230

RESULT 3
 P97823 PRELIMINARY; PRT; 230 AA.
 AC P97823;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE LYSOLECTHINASE (Phospholipase B) (Adult Male Kidney cDNA, Riken
 DE (LYSOLECTHINASE) (Phospholipase B) (Adult Male Kidney cDNA, Riken
 DE Full-length enriched library, clone:0610025N20, FULL INSERT sequence)
 DE (Lysophospholipase 1).
 GN LYP1A1 OR PLA1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang A., Deems R.A., Dennis E.A.;
 RL J. Biol. Chem. 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasekawa T., Saito R.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kaota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
 RA Blake J., Botfield D., Bojunga N., Carrinchi P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBDJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O =
 CC GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
 DR EMBL: U89352; AAB4627.1; -
 DR EMBL: AK002674; BAB22276.1; -
 DR EMBL: BC013536; AAH13536.1; -
 DR HSSP: 053547; IAUO.
 DR MGD: MGI:1344588; Lyp1a1.
 DR InterPro: IPR002106; AATRNA_ligaset1.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.

DR Pfam: PF02230; abhydrolase.2; 1.
 DR PROSITE: PS00339; AA_TRNA_LIGASE_IL_2; UNKNOWN.1.
 KW Hydrolase.
 SQ SEQUENCE 230 AA; 24687 MW; 89A2017AEFC9FAC CRC64;

Query Match 90.5%; Score 968; DB 11; Length 230;
 Best Local Similarity 81.7%; Pred. No. 3, 1e-86;
 Matches 188; Conservative 8; Mismatches 12; Indels 22; Gaps 1;

OY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRP 38
 DB 1 MCGNNMSAPMPAVPAARKATAVIFLHGLDGTGHAFAAGIKSPIHIKTCFPAVMP 60
 OY 39 VTLMNNVAMPSPWFDITIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLGGFSQ 98
 DB 61 VTLMNNMAMPSPWFDIVGLSPDSQDESGIKQAETVKALIDQEVKNIGPSNRITLGGFSQ 120
 OY 99 GGALSLYLTALTTQOKLAGVTALSLPLRXSPGPGPIGANNRDISILQCHGDDCPVLPLM 158
 DB 121 GGALSLYLTALTTQOKLAGVTALSLPLRXSPGPGPIGANNRDISILQCHGDDCPVLPLM 180
 OY 159 FGSILVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLPLPID 208
 DB 181 FGSILVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLPLPID 230

RESULT 4

P70470 PRELIMINARY; PRT; 230 AA.
 AC P70470;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Lysophospholipase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=LIVER;
 RX MEDLINE=96205961; PubMed=8631810;
 RA Sugimoto H., Hayashi H., Yamashita S.;
 RT "Purification, cDNA cloning, and regulation of lysophospholipase from rat liver."
 RL J. Biol. Chem. 271:7705-7711(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HYPOPHALAMUS;
 RX MEDLINE=98308497; PubMed=9644627;
 RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
 RA Saener M., Cheng J., Buonanno A.;
 RT "cDNA cloning and expression of a novel family of enzymes with rat calcium-independent phospholipase A2 and lysophospholipase activities."
 RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
 DR EMBL: D63885; BAA09935.1; -;
 DR EMBL: U97146; AAC63430.1; -;
 DR HSSP: Q53547; 1A00.
 DR InterPro: IPR002106; AATRNA_LigaseII.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF02230; abhydrolase.2; 1.
 DR PROSITE: PS00339; AA_TRNA_LIGASE_IL_2; UNKNOWN.1.
 SQ SEQUENCE 230 AA; 24709 MW; AAFB8C4702EAD74 CRC64;

Query Match 89.5%; Score 958; DB 11; Length 230;
 Best Local Similarity 81.7%; Pred. No. 2, 9e-85;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;
 OY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRP 38
 DB 1 MCGNNMSAPMPAVPAARKATAVIFLHGLDGTGHAFAAGIKSPIHIKTCFPAVMP 60

OY 39 VTLMNNVAMPSPWFDITIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLGGFSQ 98
 DB 61 VTLMNNMAMPSPWFDITIGLSPDSQDESGIKQAETVKALIDQEVKNIGPSNRITLGGFSQ 120
 OY 99 GGALSLYLTALTTQOKLAGVTALSLPLRXSPGPGPIGANNRDISILQCHGDDCPVLPLM 158
 DB 121 GGALSLYLTALTTQOKLAGVTALSLPLRXSPGPGPIGANNRDISILQCHGDDCPVLPLM 180
 OY 159 FGSILVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLPLPID 208
 DB 181 FGSILVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLPLPID 230

RESULT 5

O9UOF9 PRELIMINARY; PRT; 214 AA.
 ID O9UOF9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Lysophospholipase isoform.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2049367; PubMed=11042152;
 RA Zhang O.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
 RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
 RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells."
 RL Genome Res. 10:1546-1560(2000).
 DR EMBL: AF077199; AAD26994.1; -;
 DR HSSP: Q53547; 1A00.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF02230; abhydrolase.2; 1.
 SQ SEQUENCE 214 AA; 22875 MW; 63BCC806F509CE8 CRC64;

Query Match 88.7%; Score 949; DB 4; Length 214;
 Best Local Similarity 88.4%; Pred. No. 2e-84;
 Matches 191; Conservative 4; Mismatches 11; Indels 10; Gaps 2;

OY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRPVTLMNNVAMPSPWFD 52
 DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTGHAFAAIR--SSHIKTCFHAHD 58
 OY 53 IIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLGGFSOGALSLYLTALTTQO 112
 DB 59 IIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLGGFSOGALSLYLTALTTQO 118
 OY 113 KLAGVTALSLPLRXSPGPGPIGANNRDISILQCHGDDCPVLPLMFGSLTVEKLTIVN 172
 DB 119 KLAGVTALSLPLRXSPGPGPIGANNRDISILQCHGDDCPVLPLMFGSLTVEKLTIVN 178
 OY 173 PANVTFTKTEGMMHSSCOQEMDMVKOFIDKLPLPID 208
 DB 179 PANVTFTKTEGMMHSSCOQEMDMVKOFIDKLPLPID 214

RESULT 6

O77820 PRELIMINARY; PRT; 219 AA.
 ID O77820;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Calcium-independent phospholipase A2 isoform 1 (Fragment).
 OS Oryctolagus cuniculus (Rabbit).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant A., Serrero G., Bates L.M., Dai G.,
  Sasser M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with
  calcium-independent phospholipase A2 and lysophospholipase
  activities."
RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
DR EMBL: U97147; AAC63431.1; -.
DR HSSP: Q53547; IAUO.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR003179; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
FT NON_TER
SQ SEQUENCE 219 AA; 23602 MW; 3864FEDC3BC912B CRC64;

Query Match 87.4%; Score 935; DB 6; Length 219;
Best Local Similarity 85.4%; Pred. No. 4,8e-83;
Matches 187; Conservative 2; Mismatches 8; Indels 22; Gaps 1;

OY 12 AIVPARKKATAAIVFLHGLGDTG-----PVRVTLNMMVAMP 49
DB 1 ASVPAARKKATAAIVFLHGLGDTGHCWAEEAFGRSHRYICPHAFVMTLNMNAMS 60
OY 50 WPDIIIGSPDSDESGIKOAEENIKALIDOEYKNGIPSNRIILGSGGALSLEYALT 109
DB 61 WPDIIIGSPDSDESGIKOAEENIKALIDOEYKNGIPSNRIILGSGGALSLEYALT 120
OY 110 TQOKLAGVRLSLFLRLKRSFPGGPIGGANRDISIIQCHGDDCPVPLMFGSLTYEKLKT 169
DB 121 TQOKLAGVRLSLFLRLKRSFPGGPIGGANRDISIIQCHGDDCPVPLMFGSLTYEKLKT 180
OY 170 LVNPANVTFTYEGMHSSCOQCEMMOVKOFIDKLPPID 208
DB 181 LVNPANVTFTYEGMHSSCOQCEMMOVKOFIDKLPPID 219

RESULT 7
O9QYTL8 PRELIMINARY: PRT: 231 AA.
AC O9QYTL8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Lysophospholipase II.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Sugimoto H.;
RT "Rat lysophospholipase II."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB021645; BAA87911.1; -.
DR HSSP: Q53547; IAUO.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR003179; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24807 MW; 49A710C5A997C7C1 CRC64;

Query Match 67.6%; Score 723; DB 11; Length 231;
Best Local Similarity 61.6%; Pred. No. 2.4e-62;
Matches 143; Conservative 27; Mismatches 36; Indels 26; Gaps 3;

OY 1 MCGNNMSTPL---PAIVPARKKATAAIVFLHGLGDTG-----P 35
DB 1 MCGNNMSTPLIDTAATVGAETAAVIFLHGLGDTGHSWADALSTIRLPHVYICPHAF 60

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OY 36 VRPVTLNMMVAMPSPFDIIIGSPDSDESGIKOAEENIKALIDOEYKNGIPSNRIILG 95
DB 61 RIVPTLNNKMWPSWFDLMGSPPADEAGIKKAAENIKALIEHEKNIPNRIYLG 120
OY 96 FSGGALSLEYALTQOKLAGVRLSLFLRLKRSFPGGPIGGANRDISIIQCHGDDCPV 155
DB 121 FSGGALSLEYALTQOKLAGVRLSLFLRLKRSFPGGPIGGANRDISIIQCHGDDCPV 179
OY 156 PLMFGSLTYEKLTVNPANVTFTYEGMHSSCOQCEMMOVKOFIDKLPPID 207
DB 180 FVRFGALTAELKRTVTVPAVQVFTYEGMHSSCOQCEMMOVKOFIDKLPPV 231

RESULT 8
O9QYTL7 PRELIMINARY: PRT: 231 AA.
AC O9QYTL7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Lysophospholipase II (lysophospholipase 2).
GN LYPLA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99165589; PubMed=10064901;
RA Toyoda T., Sugimoto H., Yamashita S.;
RT "Sequence, expression in Escherichia coli, and characterization of
  lysophospholipase II."
RL Biochim. Biophys. Acta 1437:182-193(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
  Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
  Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
  Rauehlschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
  Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barish G.,
  Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
  Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
  Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
  Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
  Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AB009653; BAA6751.1; -.
DR HSSP: Q53547; IAUO.
DR MGD: MGI:1347000; Lypla2.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR003179; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24794 MW; E18797A17570AA97 CRC64;

Query Match 67.0%; Score 717; DB 11; Length 231;
Best Local Similarity 61.2%; Pred. No. 9.1e-62;
Matches 142; Conservative 27; Mismatches 37; Indels 26; Gaps 3;

OY 1 MCGNNMSTPL---PAIVPARKKATAAIVFLHGLGDTG-----P 35

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Db 1 MCGNTMSVPLLTDAATVSGAERETAAYIFLHGLDGTGSHMADALSTIRLPHVKYICHPAP 60
QY 36 VRPVTLMNNVAMPSPWFIDIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGG 95
Db 61 RPYVTLMNNKVMPSWFDLMGISPAPDEAGIKKAENIKALIEHEMKNGIPANRIYVLGG 120
QY 96 FSOGGALSIVTALTTOOKLAGVTALSFLLPRKSPFPGPIGGANRDISILQCHGDCDPIV 155
Db 121 FSOGGALSIVTALTCPHPLAGIVALSCLWPLHRNFPQAANGSA-KDLATLQCHGELDPMV 179
QY 156 PLMFSGSLTVEKTLKTLVPANVTFTYEGSMHSSCOQEMMDVKOFIDKLPIPI 207
Db 180 PVRFGALTAELKRSVTPARVQFTYGVHSSCPQEMAAVKEFLKLPV 231

RESULT 9
ID 095372 PRELIMINARY; PRT: 231 AA.
AC 095372:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Acyl-protein thioesterase (Lysophospholipase II).
GN D386K2.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Kuznetsov S.R., Jones T.L.Z.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Frankland J.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA; AND COLON;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098668; AAC72844.1; -
DR EMBL; AL031295; CAB40158.1; -
DR EMBL; BC017193; AAH17193.1; -
DR EMBL; BC017034; AAH17034.1; -
DR HSSP; Q35347; IAUO.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24737 MW; 813C9C71757C5135 CRC64;

Query Match 66.6%; Score 713; DB 4; Length 231;
Best Local Similarity 60.8%; Pred. No. 2.2e-61;
Matches 141; Conservative 28; Mismatches 37; Indels 26; Gaps 3;

QY 1 MCGNNMSTPL---PAIVPAARKATAAVIFLHGLGDTG-----P 35
Db 1 MCGNTMSVPLLTDAATVSGAERETAAYIFLHGLDGTGSHMADALSTIRLPHVKYICHPAP 60
QY 36 VRPVTLMNNVAMPSPWFIDIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGG 95
Db 61 RPYVTLMNNKVMPSWFDLMGISPAPDEAGIKKAENIKALIEHEMKNGIPANRIYVLGG 120
QY 96 FSOGGALSIVTALTTOOKLAGVTALSFLLPRKSPFPGPIGGANRDISILQCHGDCDPIV 155
Db 121 FSOGGALSIVTALTCPHPLAGIVALSCLWPLHRNFPQAANGSA-KDLATLQCHGELDPMV 179
QY 156 PLMFSGSLTVEKTLKTLVPANVTFTYEGSMHSSCOQEMMDVKOFIDKLPIPI 207
Db 180 PVRFGALTAELKRSVTPARVQFTYGVHSSCPQEMAAVKEFLKLPV 231

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RESULT 10
ID 09060 PRELIMINARY; PRT: 231 AA.
AC 09060:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE D3570F3.6 (novel protein similar to lysophospholipase II
DE (LYPLA2)).
GN D3570F3.6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mashreghi-Mohammadi M.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050332; CAB63783.1; -
DR HSSP; Q35347; IAUO.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24985 MW; 0C12C486013DBE8A CRC64;

Query Match 62.8%; Score 672; DB 4; Length 231;
Best Local Similarity 58.2%; Pred. No. 2.2e-57;
Matches 135; Conservative 29; Mismatches 42; Indels 26; Gaps 3;

QY 1 MCGNNMSTPL---PAIVPAARKATAAVIFLHGLGDTG-----P 35
Db 1 MCGNTMSVPLLTDAATVSGAERETAAYIFLHGLDGTGSHMADALSTIRLPHVKYICHPAP 60
QY 36 VRPVTLMNNVAMPSPWFIDIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGG 95
Db 61 RPYVTLMNNKVMPSWFDLMGISPAPDEAGIKKAENIKALIEHEMKNGIPANRIYVLGG 120
QY 96 FSOGGALSIVTALTTOOKLAGVTALSFLLPRKSPFPGPIGGANRDISILQCHGDCDPIV 155
Db 121 FSOGGALSIVTALTCPHPLAGIVALSCLWPLHRNFPQAANGSA-KDLATLQCHGELDPMV 179
QY 156 PLMFSGSLTVEKTLKTLVPANVTFTYEGSMHSSCOQEMMDVKOFIDKLPIPI 207
Db 180 PVRFGALTAELKRSVTPARVQFTYGVHSSCPQEMAAVKEFLKLPV 231

RESULT 11
ID 043202 PRELIMINARY; PRT: 104 AA.
AC 043202:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE Probable lysophospholipase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA MEDLINE-96207227; PubMed=8619474;
RA Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
RT "A double adaptor" method for improved shotgun library
RT construction.*;
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA MEDLINE-97264341; PubMed=9110174;
RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;

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"Large-scale concatenation cdna sequencing.";
 RT Genome Res. 7:353-358(1997).
 RL EMBL: AF035293; AAB8180.1; -
 DR InterPro: IPR003140; PLP_Cestrase.
 DR Pfam: PF02230; abhydrolase_2; 1.
 FT NON_TER
 SQ SEQUENCE 104 AA; 11403 MW; CB6C320EBA1011B3 CRC64;
 Query Match 46.6%; Score 499; DB 4; Length 104;
 Best Local Similarity 97.0%; Pred. No. 5,4e-41;
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 QY 110 TQOKLAGVTALSFLLPLRXSPQGPFGIGANRDISILGCHGDDPLVPLMGSLTYEKLKT 169
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 QY 170 LVNPNVTFKTYEGMHHSSCOEDMDVKQFIDKLPLPD 208
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 RESULT 12
 Q917R0 PRELIMINARY; PRT; 216 AA.
 AC Q917R0;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CG18815 protein (GH04560p).
 GN CG18815.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriil J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borzova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Pertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheibel F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spiedling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.W., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Abmayyan A., Carlson J.,
 RA Champagne R., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03544; AAC22322.1; -
 DR EMBL: AY094672; AAM11025.1; -
 DR HSSP: Q53547; 1AUO.
 DR FLYBase: FBgn0042138; CG18815.
 DR InterPro: IPR003140; PLP_Cestrase.
 DR InterPro: IPR000379; Ser_estrs.site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 SQ SEQUENCE 216 AA; 23162 MW; 456B9E0148AB7CB CRC64;
 Query Match 45.8%; Score 490; DB 5; Length 216;
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 Matches 103; Conservative 24; Mismatches 61; Indels 26; Gaps 3;
 QY 11 PAIYPAARKATAAATFPLHGLDTS-----PVRPVTNNMVAAP 48
 DB 4 PVIYEAATYKQTATILIFMHGLDTSCHSSSALAAIRPFPMKVICPTAPQVSLNAGRMP 63
 QY 49 SWFDIIGLSPDSODESGIKQANRICALIDQEVKNCIPSNRIILGFSOGGALSITVAL 108
 DB 64 SWFDIIGLIDGCPDEPGICGARDVSHVQIKETISAGIPANRIYLGFSOGGALSITVAL 123
 QY 109 TQOKLAGVTALSFLLPLRXSPQGPFGIGANRDISILGCHGDDPLVPLMGSLTYEKLKT 168
 DB 124 TYDQPLAGVALSCWLPRLHGFPGAKVN--SDVPTRQAHGDDVPVYKFGQLSLSLK 181
 QY 169 TLVNPANVTFKTYEGMHHSSCOEDMDVKQFIDKL 202
 DB 182 SFMK--NVTFTKTYGSLSHSSDDMDVDYKDIISK 213
 RESULT 13
 Q21224 PRELIMINARY; PRT; 223 AA.
 ID Q21224;
 AC Q21224;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE K04G2.5 protein.
 GN K04G2.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Gardner A.E.;
 RA Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99069613; PubMed=9851916;
 RX none;
 RA "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z75712; CAB00042.2; -
 DR InterPro: IPR003140; PLP_Cestrase.
 DR InterPro: IPR000379; Ser_estrs.site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 SQ SEQUENCE 223 AA; 24334 MW; 305C376EFD030E10 CRC64;

Query Match 39.5%; Score 422.5; DB 5; Length 223;
 Best Local Similarity 44.2%; Pred. No. 4,4e-33;
 Matches 95; Conservative 23; Mismatches 66; Indels 31; Gaps 5;

QY 11 PAIVPAAR-KATAAVIFLHGLDGTG-----PVRPTLNMNVA 47
 DB 9 PSIVSPRGEHKGTLFLHGLDGTGHWADAKTEAKHDNIKFIQHSSERPVTLNMGMRM 68
 QY 48 PSMFDITIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALSLYTA 107
 DB 69 PAMFDLGLDPAQDEDEGINRATQYHQLIDAEVAAIPASRIVAGSGALAIYAG 128
 QY 108 LTTQOKLAGVTALSLFLPLRXSPFOGPIG--ANRDISILQCHGDCDPLVPLMGSLTVE 165
 DB 129 LFTYQKLGIVGLSFLQRTKFP-----GSTANNATPIFLHGCTDPLVPLQFGQMSQ 184
 QY 166 KLKTLVNPANVTFKTEGMMHSSCOQEMMDVKOFI 200
 DB 185 YIKKF-NP-KVELHTYRGOMHSSCGEEMRDVKTFL 217

RESULT 14
 QY08F2 PRELIMINARY; PRT; 227 AA.

AC Q908F2; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Lysophospholipase.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PHILIPPINE;
 RA Fan J., Brindley P.J.;
 RT "Cloning and overexpression in Escherichia coli and immunological
 assay of a lysophospholipase homolog from Schistosoma japonicum".
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF091539; AAD52700.1; -;
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR003140; PLP_Cesterase.
 DR InterPro; IPR000379; Ser-estrs_site.
 DR Pfam; PF02230; abhydrolase_2; 1.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 SQ SEQUENCE 227 AA; 24843 MW; FE3050D50B0A753 CRC64;

Query Match 38.0%; Score 406.5; DB 5; Length 227;
 Best Local Similarity 40.5%; Pred. No. 1.6e-31;
 Matches 89; Conservative 36; Mismatches 70; Indels 25; Gaps 5;

QY 10 LPAIVPAAR-KATAAVIFLHGLDGTG-----PVRPTLNMNVA 46
 DB 6 LPAIVVASRSKHTATLFLHGLDGTGHWSDTLQYVNYFKVICPHANSIPVTLNGMC 65
 QY 47 MPMFDITIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALSLY 106
 DB 66 MPAYWDIFALSENKODEPGIKGASVELGKFAKIKAGIPVENTIVIGFSGGSVPLYN 125
 QY 107 ALTTQOKLAGVTALSLFLPLRXSPFOGPIG--IGANRDISILQCHGDCDPLVPLMGSLTVE 165
 DB 126 ALTSTLQYGGVAFSCWPLRHKFMSSPTLLTPKDVPFQCHGLDDCMIPFAMGKLTHE 185
 QY 166 KLKTLVNPANVTFKTEGMMHSSCOQEMMDVKOFI 205
 DB 186 LKKNF-QLSKCELKCYPDLSHSCCEMEDLRFELARNIP 224

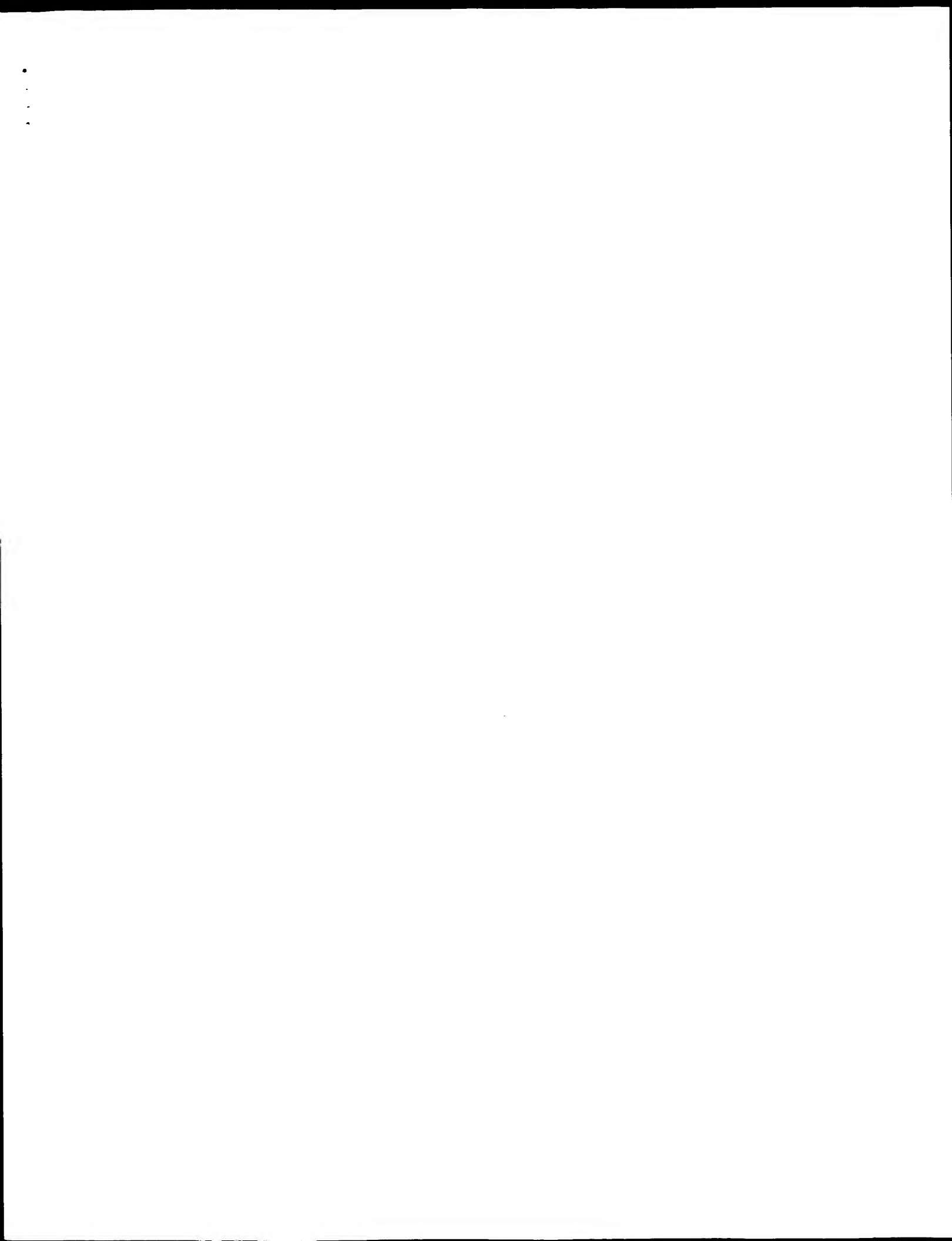
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 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Lysophospholipase homolog.
 GN SMLPLH.
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EGYPTIAN;
 RX MEDLINE=99011094; PubMed=9797070;
 RA Hamdan F.F., Ribeiro P.;
 RT "Cloning and sequence analysis of a lysophospholipase homolog from
 Schistosoma mansoni".
 RL Parasitol. Res. 84:839-842(1998).
 DR EMBL; AF066678; AAC62254.1; -;
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR003140; PLP_Cesterase.
 DR InterPro; IPR000379; Ser-estrs_site.
 DR Pfam; PF02230; abhydrolase_2; 1.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 SQ SEQUENCE 239 AA; 25870 MW; 8289D6563DC2D441 CRC64;

Query Match 38.0%; Score 406.5; DB 5; Length 239;
 Best Local Similarity 40.0%; Pred. No. 1.7e-31;
 Matches 88; Conservative 37; Mismatches 70; Indels 25; Gaps 4;

QY 10 LPAIVPAAR-KATAAVIFLHGLDGTG-----PVRPTLNMNVA 46
 DB 18 LPAIVVASRSKHTATLFLHGLDGTGHWSDALKEVPPYFIKICPHANSIPVTLNGMC 77
 QY 47 MPMFDITIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALSLY 106
 DB 78 MPAYWDIFALSENKODEPGIKGASVELGKFAKIKAGIPVENTIVIGFSGGSVPLYN 137
 QY 107 ALTTQOKLAGVTALSLFLPLRXSPFOGPIG--IGANRDISILQCHGDCDPLVPLMGSLTVE 165
 DB 138 ALTSTLQYGGVAFSCWPLRHKFMSSPTLLTPKDVPFQCHGLDXYIPFAMGKLTHE 197
 QY 166 KLKTLVNPANVTFKTEGMMHSSCOQEMMDVKOFI 205
 DB 198 LKTF-QLSKCELKCYPDLSHSCCEKEMGDILFELSKNIP 236

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 Job time : 133 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2003, 00:45:55 ; Search time 3196 Seconds

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Title: US-09-988-982-2

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IDENTITY_NUC
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Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	707.6	99.8	709	6 AR028701	AR028701 Sequence
2	707.6	99.8	709	6 AR079196	AR079196 Sequence
3	707.6	99.8	709	6 AR104346	AR104346 Sequence
4	707.6	99.8	709	6 AR178569	AR178569 Sequence
5	675.8	95.3	2408	6 AX018183	AX018183 Sequence
6	628.4	88.6	1486	6 BC008652	BC008652 Homo sapi
7	628.4	88.6	1486	6 AR079197	AR079197 Sequence
8	628.4	88.6	1486	6 AR104347	AR104347 Sequence
9	628.4	88.6	1556	6 AR203099	AR203099 Sequence
10	628.4	88.6	1556	6 AF052112	AF052112 Homo sapi
11	589.4	83.1	2417	6 AR203084	AR203084 Sequence
12	589.4	83.1	2417	6 AX256070	AX256070 Sequence
13	589.4	83.1	2417	9 AF081281	AF081281 Homo sapi
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15	572.4	80.7	760	9 AF291053	AF291053 Homo sapi
16	557.8	78.7	1381	9 BC010397	BC010397 Homo sapi
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18	473.2	66.7	660	4 OC097147	OC097147 Oryctolagus
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20	452	63.8	2356	10 RAT25KDL	D63885 Rat Liver m
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29	379.6	53.5	232728	2 AC111839	AC111839 Rattus no
30	378.4	53.4	183586	2 AC099137	AC099137 Rattus no
31	368.6	52.0	197959	2 AC118121	AC118121 Rattus no
32	325.2	45.9	154419	2 AC073054	AC073054 Homo sapi
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35	217.2	30.6	1536	10 AB021645	AB021645 Rattus no
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37	217.2	30.6	1620	9 BC017034	BC017034 Homo sapi
38	217.2	30.6	1624	6 AR113046	AR113046 Sequence
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42	209.2	29.5	94770	9 HSDJ570F3	AL050332 Human DNA
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ALIGNMENTS

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AR028701	AR028701	Sequence 2 from patent US 5858756.					
AR028701	AR028701	GI:5940674					
REFERENCE	1 (bases 1 to 709)						
AUTHORS	Hillman, J.L., Shah, P. and Murry, L.F.						
TITLE	Human lysophospholipase						
JOURNAL	Patent: US 5858756-A 2 12-JAN-1999;						
FEATURES	Location/Qualifiers						
ORGANISM	Unknown.						
SOURCE	Unknown.						
KEYWORDS	Unclassified.						

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ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTCGACGCCCTTGGGCGCGCGCGCGCGCTTCTTCCGCTTCCGCTG 60
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DB 121 CCGCCCGGAAGGCCACCGCTGCGGTATTTCTGCATGGATTGGAGATCTGGGCTG 180
QY 181 TTAGGCTGTTCATTAATATGAGTGGCTATGCTTCATGCTTGAATATATGGGC 240
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QY 361 TTTCACAGGAGAGCTTATCTTATATCTGCCCTTACACACAGCAAGAACTGGCAG 420
DB 361 TTTCACAGGAGAGCTTATCTTATATCTGCCCTTACACACAGCAAGAACTGGCAG 420
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DB 421 GTGTCACTGACACTGATTTCTTCTTCCACTTGGGNTTCTTTCACAGGKCTATCG 480
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QY 661 TCAAGCAATTCATTTGATTAACCTCTACCTCAATGATGATGATGATG 709
DB 661 TCAAGCAATTCATTTGATTAACCTCTACCTCAATGATGATGATGATGATG 709

RESULT 2
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LOCUS AR079196
DEFINITION Sequence 2 from patent US 5965423.
ACCESSION AR079196
VERSION AR079196.1 GI:10005942
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 709)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 5965423-A 2 12-OCT-1999;
FEATURES Location/Qualifiers

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BASE COUNT 166 a 169 c 175 g 197 t 2 others
ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTCGACGCCCTTGGGCGCGCGCGCGCGCTTCTTCCGCTTCCGCTG 60
DB 1 GCGGCTCGACGCCCTTGGGCGCGCGCGCGCGCTTCTTCCGCTTCCGCTG 60
QY 61 AGCTGAGGCGGTATGTGGGCAATATGCAACCCCGCTCCCGCATGTCGCCG 120
DB 61 AGCTGAGGCGGTATGTGGGCAATATGCAACCCCGCTCCCGCATGTCGCCG 120
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DB 121 CCGCCCGGAAGGCCACCGCTGCGGTATTTCTGCATGGATTGGAGATCTGGGCTG 180
QY 181 TTAGGCTGTTCATTAATATGAGTGGCTATGCTTCATGCTTGAATATATGGGC 240
DB 181 TTAGGCTGTTCATTAATATGAGTGGCTATGCTTCATGCTTGAATATATGGGC 240
QY 241 TTTCACAGATTCACAGAGAGATGAATCTGGATTAAACAGCAGCAGAAATATAAG 300
DB 241 TTTCACAGATTCACAGAGAGATGAATCTGGATTAAACAGCAGCAGAAATATAAG 300
QY 301 CTTTGATTTGATCAAGAAGTCAAGATGGCATCTTCTTAACAGATTTATTTGGAGGT 360
DB 301 CTTTGATTTGATCAAGAAGTCAAGATGGCATCTTCTTAACAGATTTATTTGGAGGT 360
QY 361 TTTCACAGGAGAGCTTATCTTATATCTGCCCTTACACACAGCAAGAACTGGCAG 420
DB 361 TTTCACAGGAGAGCTTATCTTATATCTGCCCTTACACACAGCAAGAACTGGCAG 420
QY 421 GTGTCACTGACACTGATTTCTTCTTCCACTTGGGNTTCTTTCACAGGKCTATCG 480
DB 421 GTGTCACTGACACTGATTTCTTCTTCCACTTGGGNTTCTTTCACAGGKCTATCG 480
QY 481 GTGTGCTAATATAGATATTTCTATCTCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
DB 481 GTGTGCTAATATAGATATTTCTATCTCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATGATGATTCAGCCCAATG 600
DB 541 CCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATGATGATTCAGCCCAATG 600
QY 601 TGACCTTTAAACCTATGAAGATGATGACAGTCTGTCTCAACAGGAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAAGATGATGACAGTCTGTCTCAACAGGAATGATGATG 660
QY 661 TCAAGCAATTCATTTGATTAACCTCTACCTCAATGATGATGATGATGATG 709
DB 661 TCAAGCAATTCATTTGATTAACCTCTACCTCAATGATGATGATGATGATGATG 709

RESULT 3
AR104346 709 bp DNA linear PAT 14-FEB-2001
LOCUS AR104346
DEFINITION Sequence 2 from patent US 6093561.
ACCESSION AR104346
VERSION AR104346.1 GI:12817054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 709)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 6093561-A 2 25-JUL-2000;
FEATURES Location/Qualifiers

source 1..709
/organism="unknown"
BASE COUNT 166 a 169 c 175 g 197 t 2 others
ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTGCACAGCCCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
DB 1 GCCGCTGCACAGCCCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
QY 61 AGCTAGGCGGCTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCGCATCGGCCG 120
DB 61 AGCTAGGCGGCTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCGCATCGGCCG 120
QY 121 CCGCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATACTGGGCTG 180
DB 121 CCGCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATACTGGGCTG 180
QY 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTGGGC 240
DB 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTGGGC 240
QY 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGACAGAAATATTAAG 300
DB 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGACAGAAATATTAAG 300
QY 301 CTTTGATTTGATCAAGAAATGAAGATGAGCATTCCTTCAACAGATTAATTTGGAGGT 360
DB 301 CTTTGATTTGATCAAGAAATGAAGATGAGCATTCCTTCAACAGATTAATTTGGAGGT 360
QY 361 TTTCACGAGGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
DB 361 TTTCACGAGGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
QY 421 GTGTACACTGACACTAGTTCTTGGCTCCACTTGGGANTCTTTCACAGGKCTATCG 480
DB 421 GTGTACACTGACACTAGTTCTTGGCTCCACTTGGGANTCTTTCACAGGKCTATCG 480
QY 481 GTGTGCTAATAGAGATATTTCTATTTCTCAAGTCCACAGGGGATTTGACCCCTTGGTTC 540
DB 481 GTGTGCTAATAGAGATATTTCTATTTCTCAAGTCCACAGGGGATTTGACCCCTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
DB 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGACACAGTGTGTCACAGAGAAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAGATGATGACACAGTGTGTCACAGAGAAATGATGATG 660
QY 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709
DB 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709

RESULT 4
LOCUS ARI78569 709 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6319701.
ACCESSION ARI78569
VERSION ARI78569.1 GI:20219707
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 709)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 6319701-A 2 20-NOV-2001;
FEATURES Location/Qualifiers

source 1..709
/organism="unknown"
BASE COUNT 166 a 169 c 175 g 197 t 2 others
ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTGCACAGCCCTTGGGCGCGGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
DB 1 GCCGCTGCACAGCCCTTGGGCGCGGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
QY 61 AGCTAGGCGGCTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCGCATCGGCCG 120
DB 61 AGCTAGGCGGCTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCGCATCGGCCG 120
QY 121 CCGCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATACTGGGCTG 180
DB 121 CCGCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATACTGGGCTG 180
QY 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTGGGC 240
DB 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTGGGC 240
QY 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGACAGAAATATTAAG 300
DB 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGACAGAAATATTAAG 300
QY 301 CTTTGATTTGATCAAGAAATGAAGATGAGCATTCCTTCAACAGATTAATTTGGAGGT 360
DB 301 CTTTGATTTGATCAAGAAATGAAGATGAGCATTCCTTCAACAGATTAATTTGGAGGT 360
QY 361 TTTCACGAGGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
DB 361 TTTCACGAGGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
QY 421 GTGTACACTGACACTAGTTCTTGGCTCCACTTGGGANTCTTTCACAGGKCTATCG 480
DB 421 GTGTACACTGACACTAGTTCTTGGCTCCACTTGGGANTCTTTCACAGGKCTATCG 480
QY 481 GTGTGCTAATAGAGATATTTCTATTTCTCAAGTCCACAGGGGATTTGACCCCTTGGTTC 540
DB 481 GTGTGCTAATAGAGATATTTCTATTTCTCAAGTCCACAGGGGATTTGACCCCTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
DB 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGACACAGTGTGTCACAGAGAAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAGATGATGACACAGTGTGTCACAGAGAAATGATGATG 660
QY 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709
DB 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709

RESULT 5
LOCUS AX018183 2408 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 156 from Patent WO946374.
ACCESSION AX018183
VERSION AX018183.1 GI:10042561
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2408)
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilsarsky,C.
TITLE Human nucleic acid sequences from prostate tumour tissue

QY 176 -GCCTGTAGGCGCTTTACATTAATTAAGACGTGGCTATGCTTCATGTTGATATTA 234
 DB 261 GCGCTGTAGGCGCTTTACATTAATTAAGACGTGGCTATGCTTCATGTTGATATTA 320
 QY 235 TTGGGCTTTACACAGATTCACAGAGATGAATCTGGGATTAAACAGCAGAGAAATA 294
 DB 321 TTGGGCTTTACACAGATTCACAGAGATGAATCTGGGATTAAACAGCAGAGAAATA 380
 QY 295 TAAAGCTTTGATTTGATTAAGAGATGAATGAATGATTCCTTTACAGAAATTTATTTGG 354
 DB 381 TAAAGCTTTGATTTGATTAAGAGATGAATGAATGATTCCTTTACAGAAATTTATTTGG 440
 QY 355 GAGGCTTTTTCAGAGAGAGAGCTTTATCTTATATCTGCTTACACAGAGAGAAAC 414
 DB 441 GAGGCTTTTTCAGAGAGAGAGCTTTATCTTATATCTGCTTACACAGAGAGAAAC 500
 QY 415 TTGGAGGTGTCTACCTGCTCAGTTCTTCTGCTTCCAGTTGGGANTCTTTCCACAGGKC 474
 DB 501 TTGGAGGTGTCTACCTGCTCAGTTCTTCTGCTTCCAGTTGGGANTCTTTCCACAGGKC 560
 QY 475 CTATGCGTGTGCTTAATAGATATTTCTATTTCTCCAGTGCACAGGGGATTTGACCCCTT 534
 DB 561 CTATGCGTGTGCTTAATAGATATTTCTATTTCTCCAGTGCACAGGGGATTTGACCCCTT 620
 QY 535 TTGTTCCCTGATGTTGTTGTTCTCTTACGCTGAGAAACCTAAACATTTGTTGAATCCAG 594
 DB 621 TTGTTCCCTGATGTTGTTGTTCTCTTACGCTGAGAAACCTAAACATTTGTTGAATCCAG 680
 QY 595 CCAATGTGACCTTTAAACCTATGAAGATATGATGACACAGTTGCTGTATACAGAAATGA 654
 DB 661 CCAATGTGACCTTTAAACCTATGAAGATATGATGACACAGTTGCTGTATACAGAAATGA 740
 QY 655 TTGATGTCAAGCAATTCATTTGATTAACCTCACTCCCAATGATTGATGACCTACTA 709
 DB 741 TTGATGTCAAGCAATTCATTTGATTAACCTCACTCCCAATGATTGATGACCTACTA 795

 RESULT 7
 LOCUS AR079197 1486 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 4 from patent US 5965423.
 ACCESSION AR079197
 VERSION AR079197.1 GI:10005943
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1486)
 AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
 TITLE Human lysophospholipase
 JOURNAL Patent: US 5965423-A 4 12-Oct-1999;
 FEATURES
 source 1..1486
 BASE COUNT 418 a 304 c 300 g 459 t 5 others
 ORIGIN
 Query Match 88.6%; Score 628.4; DB 6; Length 1486;
 Best Local Similarity 91.0%; Pred. No. 3.8e-155;
 Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 176 ----- 175
 DB 182 GATGGGAGAGAGCGCTTTGCAGTATCGAAGTTCAATATCAATATATCTGCCGAGT 241
 QY 176 -GCCTGTAGGCGCTTTACATTAATTAAGACGTGGCTATGCTTCATGTTGATATTA 234
 DB 242 GCGCTGTAGGCGCTTTACATTAATTAAGACGTGGCTATGCTTCATGTTGATATTA 301
 QY 235 TTGGGCTTTACACAGATTCACAGAGATGAATGATTCCTTTACAGAAATTTATTTGG 294
 DB 302 TTGGGCTTTACACAGATTCACAGAGATGAATGATTCCTTTACAGAAATTTATTTGG 361
 QY 295 TAAAGCTTTGATTTGATTAAGAGATGAATGAATGATTCCTTTACAGAAATTTATTTGG 354
 DB 362 TAAAGCTTTGATTTGATTAAGAGATGAATGAATGATTCCTTTACAGAAATTTATTTGG 421
 QY 355 GAGGCTTTTTCAGAGAGAGAGCTTTATCTTATATCTGCTTACACAGAGAGAAAC 414
 DB 422 GAGGCTTTTTCAGAGAGAGAGCTTTATCTTATATCTGCTTACACAGAGAGAAAC 481
 QY 415 TTGGAGGTGTCTACCTGCTCAGTTCTTCTGCTTCCAGTTGGGANTCTTTCCACAGGKC 474
 DB 482 TTGGAGGTGTCTACCTGCTCAGTTCTTCTGCTTCCAGTTGGGANTCTTTCCACAGGKC 541
 QY 475 CTATGCGTGTGCTTAATAGATATTTCTATTTCTCCAGTGCACAGGGGATTTGACCCCTT 534
 DB 542 CTATGCGTGTGCTTAATAGATATTTCTATTTCTCCAGTGCACAGGGGATTTGACCCCTT 601
 QY 535 TTGTTCCCTGATGTTGTTGTTCTCTTACGCTGAGAAACCTAAACATTTGTTGAATCCAG 594
 DB 602 TTGTTCCCTGATGTTGTTGTTCTCTTACGCTGAGAAACCTAAACATTTGTTGAATCCAG 661
 QY 595 CCAATGTGACCTTTAAACCTATGAAGATATGATGACACAGTTGCTGTATACAGAAATGA 654
 DB 662 CCAATGTGACCTTTAAACCTATGAAGATATGATGACACAGTTGCTGTATACAGAAATGA 721
 QY 655 TTGATGTCAAGCAATTCATTTGATTAACCTCACTCCCAATGATTGATGACCTACTA 709
 DB 722 TTGATGTCAAGCAATTCATTTGATTAACCTCACTCCCAATGATTGATGACCTACTA 776

 RESULT 8
 LOCUS AR104347 1486 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 4 from patent US 6093561.
 ACCESSION AR104347
 VERSION AR104347.1 GI:12817055
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1486)
 AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
 TITLE Human lysophospholipase
 JOURNAL Patent: US 6093561-A 4 25-JUN-2000;
 FEATURES
 source 1..1486
 BASE COUNT 418 a 304 c 300 g 459 t 5 others
 ORIGIN
 Query Match 88.6%; Score 628.4; DB 6; Length 1486;
 Best Local Similarity 91.0%; Pred. No. 3.8e-155;
 Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 121 CGCCCGGAAGGCGACCGCTGGGATTTCTCATGATTTGGAGATACG----- 175
 DB 122 CGCCCGGAAGGCGACCGCTGGGATTTCTCATGATTTGGAGATACG----- 181
 QY 176 ----- 175
 DB 182 GATGGCAGAGAGCTTTGAGATATCAGAGATTCACATATCAATATATCTGCGCCGATG 241
 QY 176 -GCCCTTAGGCTGTATCATTAATATATGAGCTGCTATGCTTCATGCTTTGATATTA 234
 DB 242 CGCCTGTAGGCTGTATCATTAATATATGAGCTGCTATGCTTCATGCTTTGATATTA 301
 QY 235 TTGGGCTTTCACAGATTCACAGAGATGAATCTGGGTTAAACAGGAGAGAAATA 294
 DB 302 TTGGGCTTTCACAGATTCACAGAGATGAATCTGGGTTAAACAGGAGAGAAATA 361
 QY 295 TAAAGCTTTGATTTGATTCAGAGATGAGATGGCATTCCTTCTTAACAGATTTATTTGG 354
 DB 362 TAAAGCTTTGATTTGATTCAGAGATGAGATGGCATTCCTTCTTAACAGATTTATTTGG 421
 QY 355 GAGGCTTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 414
 DB 422 GAGGCTTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 481
 QY 415 TGGCAGGTGTCACTGACACTGAGTTCTTGTCTCAGCTGGGNTCTTCCACAGAGGKC 474
 DB 482 TGGCAGGTGTCACTGACACTGAGTTCTTGTCTCAGCTGGGNTCTTCCACAGAGGKC 541
 QY 475 CTATCGGTGTCTTAATAGAGATTTCTATCTCCAGTGCAGCGGAGATTTGACCCCTT 534
 DB 542 CTATCGGTGTCTTAATAGAGATTTCTATCTCCAGTGCAGCGGAGATTTGACCCCTT 601
 QY 535 TGGTCCCTCATGATTTGCTTCTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 594
 DB 602 TGGTCCCTCATGATTTGCTTCTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 661
 QY 595 CCAATGTGACCTTTAAACCTATGAGGTATGATGACAGAGTGTGTCACAGAGAAATGA 654
 DB 662 CCAATGTGACCTTTAAACCTATGAGGTATGATGACAGAGTGTGTCACAGAGAAATGA 721
 QY 655 TGGATGTCAAGCAATTCATTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 709
 DB 722 TGGATGTCAAGCAATTCATTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 776

RESULT 9
 AR203099 1556 bp DNA linear PAT 20-JUN-2002
 LOCUS AR203099 Sequence 18 from patent US 6365354.
 ACCESSION AR203099
 VERSION AR203099.1 GI:21499401
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 1556)
 AUTHORS Bennett,C.Frank, and Wyatt,J.
 TITLE Antisense modulation of lysophospholipase I expression
 JOURNAL Patent: US 6365354-A 18 02-Apr-2002;
 FEATUERS Location/Qualifiers
 source 1..1556
 /organism="unknown"

BASE COUNT 423 a 324 c 350 g 459 t
 ORIGIN
 Query Match 88.6%; Score 628.4; DB 6; Length 1556;
 Best Local Similarity 91.0%; Pred. No. 3.8e-155;
 Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 1 GCGGCTCGACGCGCTTTGGGCGCGGCGCGGCGCTTCCCTCGCTGGCGCTGG 60
 DB 121 GCGGCTCGACGCGCTTTGGGCGCGGCGCGGCGCGCTTCCCTCGCTGGCGCTGG 180

QY 61 AGCTGAGCGGCTGTATGTGCGCAATATCATGTCACACCCCGCTGCCCGCTGCCG 120
 DB 181 AGCTGAGCGGCTGTATGTGCGCAATATCATGTCACACCCCGCTGCCCGCTGCCG 240
 QY 121 CGCCCGGAAGGCGACCGCTGGGATTTCTCATGATTTGGAGATACG----- 175
 DB 241 CGCCCGGAAGGCGACCGCTGGGATTTCTCATGATTTGGAGATACG----- 300
 QY 176 ----- 175
 DB 301 GATGGCAGAGAGCTTTGAGATATCAGAGATTCACATATCAATATATCTGCGCCGATG 360
 QY 176 -GCCCTTAGGCTGTATCATTAATATATGAGCTGCTATGCTTCATGCTTTGATATTA 234
 DB 361 CGCCTGTAGGCTGTATCATTAATATATGAGCTGCTATGCTTCATGCTTTGATATTA 420
 QY 235 TTGGGCTTTCACAGATTCACAGAGATGAATCTGGGTTAAACAGGAGAGAAATA 294
 DB 421 TTGGGCTTTCACAGATTCACAGAGATGAATCTGGGTTAAACAGGAGAGAAATA 480
 QY 295 TAAAGCTTTGATTTGATTCAGAGATGAGATGGCATTCCTTCTTAACAGATTTATTTGG 354
 DB 481 TAAAGCTTTGATTTGATTCAGAGATGAGATGGCATTCCTTCTTAACAGATTTATTTGG 540
 QY 355 GAGGCTTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 414
 DB 541 GAGGCTTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 600
 QY 415 TGGCAGGTGTCACTGACACTGAGTTCTTGTCTCAGCTGGGNTCTTCCACAGGKC 474
 DB 601 TGGCAGGTGTCACTGACACTGAGTTCTTGTCTCAGCTGGGNTCTTCCACAGGKC 660
 QY 475 CTATCGGTGTCTTAATAGAGATTTCTATCTCCAGTGCAGCGGAGATTTGACCCCTT 534
 DB 661 CTATCGGTGTCTTAATAGAGATTTCTATCTCCAGTGCAGCGGAGATTTGACCCCTT 720
 QY 535 TGGTCCCTCATGATTTGCTTCTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 594
 DB 721 TGGTCCCTCATGATTTGCTTCTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 780
 QY 595 CCAATGTGACCTTTAAACCTATGAGGTATGATGACAGAGTGTGTCACAGAGAAATGA 654
 DB 781 CCAATGTGACCTTTAAACCTATGAGGTATGATGACAGAGTGTGTCACAGAGAAATGA 840
 QY 655 TGGATGTCAAGCAATTCATTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 709
 DB 841 TGGATGTCAAGCAATTCATTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 895

RESULT 10
 AF052112 1556 bp mRNA linear PRI 05-AUG-1998
 LOCUS AF052112 Homo sapiens clone 23753 mRNA sequence.
 DEFINITION AF052112
 ACCESSION AF052112
 VERSION AF052112.1 GI:3360419
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1556)
 AUTHORS Anderson,B., Wentland,M.A., Ricafente,J.Y., Liu,W., and Gibbs,R.A.
 TITLE A 'double adaptor' method for improved shotgun library construction
 JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)
 MEDLINE 96207227
 PUBMED 8619474
 2 (bases 1 to 1556)
 AUTHORS Yu,W., Anderson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.,
 Ricafente,J.Y., Wentland,M.A., Lennon,G., and Gibbs,R.A.
 TITLE Large-scale concatenation cDNA sequencing
 JOURNAL Genome Res. 7 (4), 353-358 (1997)
 MEDLINE 97264341
 PUBMED 9110174


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Db      661 GTTCGTCAACAGAAATGATGATGTCAGCAATTCATTAATCTCACTCCAA 720
QY      694 TTGATTGAGTCACCTA 709
        |||||||
Db      721 TTGATTGAGTCACCTA 736

RESULT 12
AX256070
LOCUS    AX256070          2417 bp    DNA        linear    PAT 10-OCT-2001
DEFINITION Sequence 221 from Patent WO0170976.
ACCESSION AX256070
VERSION   AX256070.1 GI:16075110
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2417)
AUTHORS   Xu,J., Pyle,R.A. and Stolk,J.A.
TITLE     Compositions and methods for the therapy and diagnosis of ovarian
           and endometrial cancer
JOURNAL   Patent: WO 0170976-A 221 27-SEP-2001;
           CORIXA CORPORATION (US)
FEATURES
           source          1..2417
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
BASE COUNT 752 a 414 c 422 g 829 t
ORIGIN

Query Match      83.1%; Score 589.4; DB 6; Length 2417;
Best Local Similarity 90.5%; Pred. No. 8.2e-145;
Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY      40 CTTCCTTCGGCTTGGCTGTGAGCTGAGCGGCTGTATGTGGCGCAATAATGTCACACC 99
        |||||||
Db      1 CTTCCTTCGGCTTGGCTGTGAGCTGAGCGGCTGTATGTGGCGCAATAATGTCACACC 60

QY      100 CGGTGCCCCCATCGTGGCCGCCGCCGCGGAGAGCCACCGCTGGGATTTCTTCGTCATG 159
        |||||||
Db      61 CGGTGCCCCCATCGTGGCCGCCGCCGCGGAGAGCCACCGCTGGGATTTCTTCGTCATG 120

QY      160 GATTGGAGACTACTG----- 175
        |||||||
Db      121 GATTGGAGACTACTGCGACGAGATGGGAGAGCCTTTCAGAGTATCAGAAAGTTCACATA 180
        |||||||
QY      176 -----GCTGTAGGCGCTGTACATTAATATGAACGTGGCTA 213
        |||||||
Db      181 TCAAAATATATCTGCCCGCATGCGCTGTAGGCGCTGTACATTAATATGAACGTGGCTA 240

QY      214 TGCCTTCATGCTTTGATTTATTTGGGCTTTCACAGATTTACAGAGAGTGAATCTGGGA 273
        |||||||
Db      241 TGCCTTCATGCTTTGATTTATTTGGGCTTTCACAGATTTACAGAGAGTGAATCTGGGA 300

QY      274 TTAACAGGACAGAAAAATATAAAGCTTTGATTGATCAAGAAAGTGAAGATGGCATTC 333
        |||||||
Db      301 TTAACAGGACAGAAAAATATAAAGCTTTGATTGATCAAGAAAGTGAAGATGGCATTC 360

QY      334 CTTCTACAGAAATATTTTGGGAGGTTTTCACAGGAGAGAGCTTTATCTTTATCTAGT 393
        |||||||
Db      361 CTTCTACAGAAATATTTTGGGAGGTTTTCACAGGAGAGAGCTTTATCTTTATCTAGT 420

QY      394 CCCTTACACAGAGAGAAACTGAGAGGTCTACAGCACTAGTCTTCTGCTCCACTTC 453
        |||||||
Db      421 CCCTTACACAGAGAGAAACTGAGAGGTCTACAGCACTAGTCTTCTGCTCCACTTC 480

QY      454 GGGATTCCTTTCACAGAGGCTATCGGTGAGTAAATAGAGATTTCTATCTCCAGT 513
        |||||||
Db      481 GGGATTCCTTTCACAGAGGCTATCGGTGAGTAAATAGAGATTTCTATCTCCAGT 540

QY      514 GCCACGGGATTTGACCCCTTGGTCCCTGATGTTGGTCTCTTACGGTGGAAAAAC 573
        |||||||

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Db      541 GCCACGGGATTTGACCCCTTGGTCCCTGATGTTGGTCTCTTACGGTGGAAAAAC 600
QY      574 TAAACATTTGGTGAATCCAGCAATGAGCTTTAAACCTATGAAGATGATGACACA 633
        |||||||
Db      601 TAAACATTTGGTGAATCCAGCAATGAGCTTTAAACCTATGAAGATGATGACACA 660

QY      634 GTTCGTCAACAGAAATGATGATGTCAGCAATTCATTAATCTCACTCCAA 693
        |||||||
Db      661 GTTCGTCAACAGAAATGATGATGTCAGCAATTCATTAATCTCACTCCAA 720

QY      694 TTGATTGAGTCACCTA 709
        |||||||
Db      721 TTGATTGAGTCACCTA 736

RESULT 13
AF081281
LOCUS    AF081281          2417 bp    mRNA        linear    PRI 13-AUG-1998
DEFINITION Homo sapiens lysophospholipase (LpL1) mRNA, complete cds.
ACCESSION AF081281
VERSION   AF081281.1 GI:3415122
KEYWORDS
SOURCE    Homo sapiens.
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2417)
AUTHORS   Hu,G.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-1998) Shanghai Institute of Cell Biology, 320
           Yue-Yang Road, Shanghai 200031, China
FEATURES
           source          1..2417
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
           gene          1..2417
                        /gene="LpL1"
                        /gene="LpL1"
                        /gene="LpL1"
                        /codon_start=1
                        /product="Lysophospholipase"
                        /protein_id="AAC31610.1"
                        /translation="MCGNNMSTPLPAIVPAARKATPAVIFLGLDPTGHMAEAFAGI
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Query Match      83.1%; Score 589.4; DB 9; Length 2417;
Best Local Similarity 90.5%; Pred. No. 8.2e-145;
Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

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Db      1 CTTCCTTCGGCTTGGCTGTGAGCTGAGCGGCTGTATGTGGCGCAATAATGTCACACC 60

QY      100 CGGTGCCCCCATCGTGGCCGCCGCCGCGGAGAGCCACCGCTGGGATTTCTTCGTCATG 159
        |||||||
Db      61 CGGTGCCCCCATCGTGGCCGCCGCCGCGGAGAGCCACCGCTGGGATTTCTTCGTCATG 120

QY      160 GATTGGAGACTACTG----- 175
        |||||||
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QY      176 -----GCTGTAGGCGCTGTACATTAATATGAAGTGAAGTGGCTA 213
        |||||||
Db      181 TCAAAATATATCTGCCCGCATGCGCTGTAGGCGCTGTACATTAATATGAAGTGGCTA 240

QY      214 TGCCTTCATGCTTTGATTTATTTGGGCTTTCACAGATTTACAGAGAGTGAATCTGGGA 273
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Db 241 TGCCTTACGGTTGATATATATGGGCTTTCACCAGATTACAGAGAGATGAATCTGGGA 300
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 QY 334 CTCTAACAGAAATATTTTGGAGGCTTTCTCAGAGAGAGAGCTTTATCTTATATCTG 393
 Db 361 CTCTAACAGAAATATTTTGGAGGCTTTCTCAGAGAGAGAGCTTTATCTTATATCTG 420
 QY 394 CCCTTACACAGACGAGAACTGGCAGGTGTCAGTCACTGACATGCTTCTGCTCCACTTC 453
 Db 421 CCCTTACACAGACGAGAACTGGCAGGTGTCAGTCACTGACATGCTTCTGCTCCACTTC 480
 QY 454 GGGATTCCTTTCCACAGGAGGCTATCGGTGCTTAATAGATATTTCTATCTCCAGT 513
 Db 481 GGGCTTCCTTCCACAGGAGGCTATCGGTGCTTAATAGATATTTCTATCTCCAGT 540
 QY 514 GCCACGGGATTTGATACCTTTGGTTCCTGATGTTGGTTCCTTACGGTGGAAAAAC 573
 Db 541 GCCACGGGATTTGATACCTTTGGTTCCTGATGTTGGTTCCTTACGGTGGAAAAAC 600
 QY 574 TAAACATTTGGTGAATCCAGCAATGTGACCTTTAAAACTATGAAGATGATGACACA 633
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 QY 634 GTTCTGTCAACAGAAATGATGATGTCAGCAATTTATGATTAATCTTACTCTCA 693
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 Db 721 TTGATTGACGTCACTA 736

RESULT 14
 AL365267 49616 bp DNA linear PRI 16-OCT-2000
 LOCUS Human DNA sequence from clone RP11-789A7 on chromosome 6, complete
 DEFINITION sequence.
 ACCESSION AL365267
 VERSION AL365267.11 GI:10862783
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 49616)
 AUTHORS Williams, S.
 JOURNAL Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 Direct submission
 Requests: clonerequests@sanger.ac.uk
 On Oct 17, 2000 this sequence version replaced gi:10798380.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.

The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
 on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping

Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6>
 RP11-789A7 is from the library RPCT-11.3 constructed at the Roswell
 Park Cancer Institute by the group of Pieter de Jong. For further
 details see <http://bacpac.med.buffalo.edu/>
 VECTOR: pBACE3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-789A7. It may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true right end of clone RP11-789A7 is at 49616 in this
 sequence. The true right end of clone RP1-20N4 is at 100 in this
 sequence.

FEATURES

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 3144..3283
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 3638..3714
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 10693..10791
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misc_feature		complement(22534. .23017)
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repeat_region		/note="L1M4 repeat: matches 2418. .3266 of consensus"
repeat_region	24857. .25412	
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repeat_region	25413. .25716	
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repeat_region	25717. .25986	
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repeat_region	25985. .26650	
repeat_region		/note="L1MD repeat: matches 0. .970 of consensus"
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repeat_region	30162. .30324	
repeat_region		/note="MER3 repeat: matches 3. .169 of consensus"
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repeat_region	34269. .34424	
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Best Local Similarity	88.7%; Pred. No. 2..2e-142;
Mismatches 689; Conservative	1; Mismatches 19; Indels 69; Gaps 3

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QY	176	-----	175
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QY	534	TTGGTTCCCGGTATGTTGGTTCTCTTACGGTGGAAAAACT-AAAAATTTGGTAATCC	592
Db	17883	TTGGTTCCCGGTATGTTGGTTCTCTTACGGTGGAAAAACTAAAAAATTTGGTAAATCC	17942
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Db	17943	AGCCAAATGACCTTTAAACCACTATGAAGGTATGTGTGCACAGTTGCTGTCAACAGGAAT	18002
QY	653	GATGATGTCAAGCAATTCATTGATTAACCTCTACCTCCAATTGATTGACGTCACTA	709

Db 18003 GATGAATGTCAGCAATTCATTGATTAACCTCCTACCTCCATTGATTGACGTCACTA 18059

RESULT 15

AF291053 760 bp mRNA linear PRI 20-NOV-2000

LOCUS AF291053 Homo sapiens acyl-protein thioesterase-1 mRNA, complete cds.

DEFINITION AF291053

ACCESSION AF291053.1 GI:9965371

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 760)

AUTHORS Deryudjev, Y., Dauter, Z., Kuznetsov, S.R., Jones, T.L. and Deryudjeva, Z.S.

TITLE Crystal structure of the human acyl protein thioesterase I from a single X-ray data set to 1.5 Å

JOURNAL MEDLINE 20535036

PubMed 11080636

REFERENCE 2 (bases 1 to 760)

AUTHORS Kuznetsov, S.R. and Jones, T.L.Z.

TITLE Direct Submission

JOURNAL Submitted (28-JUL-2000) Metabolic Disease Branch, National Institute of Diabetes and Digestive and Kidney Diseases, 9000 Rockville Pike, Bldg.10, Room 9C112, Bethesda, MD 20892, USA

FEATURES

source location/Qualifiers

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19..711

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BASE COUNT 197 a 166 c 186 g 211 t

ORIGIN

Query Match 80.7%; Score 572.4; DB 9; Length 760;

Best Local Similarity 90.3%; Pred. No. 2,2e-140;

Matches 649; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

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DB 1 TGTGAGCTGAGGCGGTGATGTGCGGCAATAACATGTCACCCGCTGCCCATGCTG 60

OY 117 CCGCGCGCGCGGAGGAGCCACCGCTGCGGTGATTTCCCTGCAATGATTGGAGATACTGG- 175

DB 61 CCGCGCGCGCGGAGGAGCCACCGCTGCGGTGATTTCCCTGCAATGATTGGAGATACTGGG 120

OY 176 ----- 175

DB 121 CACGATGGGCAAGACCTTTGCGAGGTATCAGAAGTTCACATATCAATATATCTGCCCG 180

OY 176 -----GCCTGTAGGCTGTATACATTAATATGAACGTGCTATGCTTCATGCTTTGAT 230

DB 181 CATGGCCTGTAGGCTGTATACATTAATATGAACGTGCTATGCTTCATGCTTTGAT 240

OY 231 ATTATTGGGCTTTCACCATTCACAGAGATGATCTGGGATTAAACAGGACGAGAA 290

DB 241 ATTATTGGGCTTTCACCATTCACAGAGATGATCTGGGATTAAACAGGACGAGAA 300

OY 291 AATAAAGCTTTGATTGATGATCAGAGAGTGAAGATGGCATTCCTCTCTAACAGAAATATT 350

DB 301 AATAAAGCTTTGATTGATGATCAGAGAGTGAAGATGGCATTCCTCTCTAACAGAAATATT 360

OY 351 TTGGAGGCTTTTCTCAGGAGGAGGAGCTTTATCTTTATATACTGCCCTTACACAGACAG 410

DB 361 TTGGAGGCTTTTCTCAGGAGGAGGAGCTTTATCTTTATATACTGCCCTTACACAGACAG 420

OY 411 AAATGCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 470

DB 421 AAATGCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

OY 471 GGCCTATCGGTGGTGGTAAATAGAGATATTCTTCTCCAGTGGCCACGGGAGATTGGAC 530

DB 481 GGCCTATCGGTGGTGGTAAATAGAGATATTCTTCTCCAGTGGCCACGGGAGATTGGAC 540

OY 531 CTTTGGTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 590

DB 541 CTTTGGTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

OY 591 CCAGCCAAATGTGACCTTTAAACCTATGAAAGTATGACACAGTGTGTCAACAGGAA 650

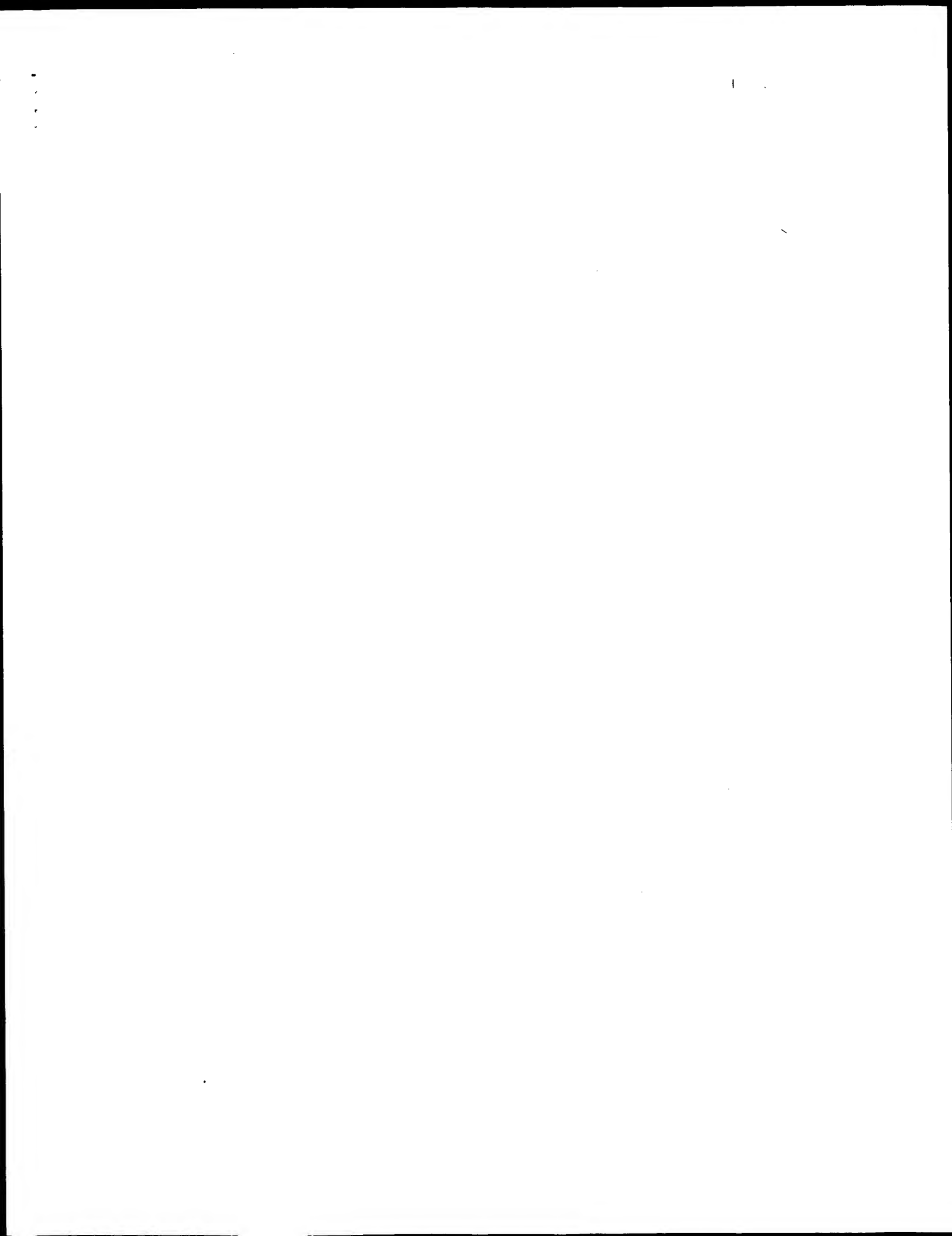
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OY 651 ATGATGATGTCAGCAATTCATGATTAACCTCCTACCTCAATGATGACGTCACCTA 709

DB 661 ATGATGATGTCAGCAATTCATGATTAACCTCCTACCTCAATGATGATGACGTCACCTA 719

Search completed: January 19, 2003, 02:36:49

Job time : 3220 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2003, 23:46:20 ; Search time 301 Seconds
(without alignments)
E001 EAT wildtype

Title: US-09-988-982-2

Perfect score: 709
Sequence: 1 GCCGCTGCACGCCCTTGG.....CCAATTGATTGACGTCACTA 709

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%

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- 24: /SID52/gcgdata/genseq/genseqn.emb1/NA2002.DAT.*

SUMMARIES

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2	663	93.5	2396	22	AAH34424	Human colon cancer
3	628.4	88.6	1486	20	AAK55267	Human lysophospho
4	628.4	88.6	1556	24	ABK37045	DNA encoding humata
5	628.4	88.6	2493	21	AAC98208	Human colon cancer
6	628.4	88.6	2600	23	ABV25207	Human prostate exp
7	606.4	85.5	1538	23	AAK71464	DNA encoding novel
8	600.8	84.7	758	22	AAH26336	Human brain lysop
9	589.4	83.1	2417	22	AAK556597	Human cDNA for an

10	589.4	83.1	2417	24	ABL75514	Human lysophospholipid
11	589.4	83.1	2417	24	ABL75514	Human encoding human
12	561	79.1	1300	21	AAZ615501	CDNA encoding a hu
13	436	61.5	693	24	ABK37037	DNA encoding mouse
14	433.2	61.1	727	24	ABK37048	DNA encoding mouse
15	392.6	55.4	419	24	ABL37708	Human colon tumour
16	217.2	30.6	164	22	AAC60229	Human hydrolase-11
17	217.2	30.6	1647	24	ABL55535	Human lysophosphol
18	164	23.1	270	23	AAST71463	DNA encoding novel
19	130	18.3	1183	20	AAZ33516	Human prostate can
20	126	17.8	782	22	AA556596	Human CDNA for an
21	119.8	16.9	461	22	AA556583	Human CDNA for an
22	97.8	13.8	363	21	AAH31022	Human colon cancer
23	93.4	13.2	1208	23	ABL21049	Drosophila melanog
24	90.6	12.8	608	24	ABK37047	DNA encoding mouse
25	88	12.4	3917	23	ABL21048	Drosophila melanog
26	64.2	9.1	62909	22	AAE28545	Genomic Fragment #
27	57.6	8.1	545	21	AAFI1497	Aspergillus oryzae
28	55.8	7.9	589	24	ABL65843	Pancreas cancer re
29	55.8	7.9	709	24	ABK34374	Human CDNA for nov
30	55.8	7.9	852	21	AAA87713	Secreted protein e
31	55.8	7.9	852	21	AAA87762	Human secreted pro
32	55.8	7.9	852	21	AAAC00014	Human secreted pro
33	55.8	7.9	852	21	AAZ42253	Human lysophosphol
34	55.8	7.9	852	22	AAE64395	CDNA encoding secr
35	55.8	7.9	852	22	AAE64044	CDNA encoding huma
36	55.8	7.9	975	20	AAX06946	Human lysophosphol
37	55.8	7.9	1861	23	ABV24194	Human prostate exp
38	55.8	7.9	1861	23	ABV25125	Human prostate exp
39	55.4	7.8	65	24	ABN55308	Mouse spliced tran
40	53.4	7.5	528	24	ABO76633	Human MBDT encodin
41	51.8	7.3	604	24	ABO56978	Human colon cancer
42	40.4	5.7	273	20	AAK40388	Human secreted pro
43	39.2	5.5	769	23	ABL11351	Drosophila melanog
44	39.2	5.5	2672	23	ABL07892	Drosophila melanog
45	39.2	5.5	2769	23	ABL11350	Drosophila melanog

ALIGNMENTS

XX	RESULT 1	
XX	AAK56266	
XX	AAK56266 standard; cDNA; 709 BP.	
AC	AAK56266;	
DT	19-JUL-1999 (first entry)	
XX		
DE	Human lysophospholipase NHLP encoding cDNA.	
XX		
KW	Human: lysophospholipase; NHLP; cell proliferation; arteriosclerosis;	
KW	atherosclerosis; buritis; cirrhosis; hepatitis; myelofibrosis;	
KW	mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;	
KW	polycythaemia vera; psoriasis; primary thrombocytopenia; cancer;	
KW	inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;	
KW	immune response; ankylosing spondylitis; autoimmune haemolytic anaemia;	
ss.		
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	75..709
FT		/*tag= a
FT		/product= "NHLP"
FT		/note= "no stop codon given"
XX		
PN	W09849319-A1.	
XX		
PD	05-NOV-1998.	
XX		
PF	29-APR-1998;	98MO-US08782.
XX		

12-FEB-1998: 98US-0022940.
 PR 29-APR-1997: 97US-0844120.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Murry LE, Shah P;
 XX
 DR WPI: 1999-3326512/27.
 DR P-PSDB; AAY09530.
 XX
 XX New human lysophospholipase (NHLP) polypeptides and polynucleotides
 PT which identify and encode NHLP
 XX
 PS Claim 7; Fig 1; 66pp; English.
 XX
 CC The present sequence encodes human lysophospholipase (NHLP). The present
 CC invention also describes a method for treating or preventing a disorder
 CC of cell proliferation (e.g. arteriosclerosis, atherosclerosis, bursts,
 CC cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,
 CC paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis,
 CC primary thrombocytopenia, and cancers), inflammation (e.g. Addison's
 CC disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a
 CC disorder of the immune response (e.g. AIDS, allergies, ankylosing
 CC spondylitis, autoimmune haemolytic anaemia) by administering an
 CC antagonist to NHLP. NHLP proteins, antagonists, antibodies, agonists,
 CC complementary sequences or vectors may be administered in combination
 CC with other therapeutic agents. Antibodies which specifically bind to
 CC NHLP may be used for the diagnosis of disorders characterized by
 CC expression of NHLP or in assays to monitor patients being treated with
 CC NHLP or agonists. The polynucleotides (PNS) encoding NHLP or fragments
 CC may be used therapeutically. In one aspect, the complement of the
 CC polynucleotides may be used where it would be desirable to block the
 CC transcription of the mRNA. Complementary molecules may be used to
 CC modulate NHLP activity or to achieve regulation of gene activity.
 CC Diagnostically, the PNS may be used to detect and quantitate gene
 CC expression in biopsied tissues in which expression of NHLP may be
 CC correlated with disease.
 CC
 CC Sequence 709 BP; 166 A; 169 C; 175 G; 197 T; 2 other;

Query Match	99.8%	Score 707.6	DB 20	Length 709
Best Local Similarity	100.0%	Pred. No. 6.2e-216		
Matches 709	Conservative	0	Mismatches 0	Indels 0
				Gaps 0
QY	1	GCGCCTGCACGCCCTTTGGGCGCGGCGGCGGCCCGCTCTTCCTCCGTCCGCTTGGCGCTGTG	60	
Db	1	GCCGCTTGCAAGCCCTTTGGGCGCGGCGGCCCGGCCCGCTCTTCCTCCGTCCGCTTGGCGCTGTG	60	
QY	61	AGCTGAGGCGGTGTATGTGGCGCAATAATATGCAACCCGCTCGCCGCCATCGTGCCCG	120	
Db	61	AGCTGAGGCGGTGTATGTGGCGCAATAATATGCAACCCGCTCGCCGCCATCGTGCCCG	120	
QY	121	CCGCGCGGAAGGCCACCGCTGGCGGTGATTTTCCTCATGATGTGGGAGATCTGGGCGTG	180	
Db	121	CCGCGCGGAAGGCCACCGCTGGCGGTGATTTTCCTCATGATGTGGGAGATCTGGGCGTG	180	
QY	181	TTAGGCGCTGTATCAATTAATAATGAAAGCGGCGATACGCTTCAGGTTTGATATTAATTTGGG	240	
Db	181	TTAGGCGCTGTATCAATTAATAATGAAAGCGGCGATACGCTTCAGGTTTGATATTAATTTGGG	240	
QY	241	TTTCACCAAGTTCACAGAGAGATGTAATCTGGGATTTAAACAGGACGACGAGAAATTTAAAG	300	
Db	241	TTTCACCAAGTTCACAGAGAGATGTAATCTGGGATTTAAACAGGACGACGAGAAATTTAAAG	300	
QY	301	CTTTGATTTGATCAAGAAAGTGAAGAAATGGCATTCCTTTCAAGAAATTAATTTTGGGAGGTT	360	
Db	301	CTTTGATTTGATCAAGAAAGTGAAGAAATGGCATTCCTTTCAAGAAATTAATTTTGGGAGGTT	360	
QY	361	TTTCTCAGGAGAGAGCTTTATCTTTTATATACGCTTACACACACAGCAAGAACTGGCAG	420	
Db	361	TTTCTCAGGAGAGAGCTTTATCTTTTATATACGCTTACACACACAGCAAGAACTGGCAG	420	
QY	421	GTGTACTGCATCAGTTTCTTGCTCCACTTGGGNTTCTTTTCCACAGGKCTATCG	480	

[illegible]

RESULT 2
 AAH34424
 ID AAH34424 standard; cDNA; 2396 BP.
 XX
 AC AAH34424:
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1506.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000MO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 DR WPI; 2001-235357/24.
 DR P-PSDB; AAG75019.
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PS useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 1; Page 3165-3166; 9803pp; English.
 CC
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were

CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 2396 BP; 767 A; 402 C; 408 G; 816 T; 3 other;

Query Match 93.5%; Score 663; DB 22; Length 2396;

Best Local Similarity 99.0%; Pred. No. 2.5e-201;

Matches 663; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

QY 40 CTTCTTCCTGCGCTGAGCTGAGCGGCTGATGCGGCATTAACATGCAACC 99
    |||
DB 1 CTTCTTCCTGCGCTGAGCTGAGCGGCTGATGCGGCATTAACATGCAACC 60
    |||
QY 100 CGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 159
    |||
DB 61 CGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
    |||
QY 160 GATTGGAGATGCTGGGCTGTTAGGCTGTTACATTAATGAACGCTATGCTT 219
    |||
DB 121 GATTGGAGATGCTGGGCTGTTAGGCTGTTACATTAATGAACGCTATGCTT 180
    |||
QY 220 CATGCTTGTATTTATTTGGGCTTTCACAGATTCACAGAGATGAATCGGATTAAC 279
    |||
DB 181 CATGCTTGTATTTATTTGGGCTTTCACAGATTCACAGAGATGAATCGGATTAAC 240
    |||
QY 280 AGGAGAGAGAAATATATAAGCTTTGATTTGATTCAGAGAGAGATGAATCGGATTAAC 339
    |||
DB 241 AGGAGAGAGAAATATATAAGCTTTGATTTGATTCAGAGAGAGATGAATCGGATTAAC 300
    |||
QY 340 ACAGAAATTTATTTGGAGGCTTTCTCAGGAGAGGCTTTATCTTTATATAGTCCCTTA 399
    |||
DB 301 ACAGAAATTTATTTGGAGGCTTTCTCAGGAGAGGCTTTATCTTTATATAGTCCCTTA 360
    |||
QY 400 CCACACAGCAGAAACTGGCAGGTCTCAGTCACTCACTTCTTCTTCCACTTCGGGNTT 459
    |||
DB 361 CCACACAGCAGAAACTGGCAGGTCTCAGTCACTCACTTCTTCTTCCACTTCGGGNTT 420
    |||
QY 460 CTTTTCACAGAGGCTTCATGGTGTCTAATAGATATTTCTATCTTCAGTCCAGGCGCAG 519
    |||
DB 421 CTTTTCACAGAGGCTTCATGGTGTCTAATAGATATTTCTATCTTCAGTCCAGGCGCAG 480
    |||
QY 520 GGGATTTGACCCCTTTGGTTCCTCGATGTTGTTGCTCTTACAGTGAGAAACTATAAAA 579
    |||
DB 481 GGGATTTGACCCCTTTGGTTCCTCGATGTTGTTGCTCTTACAGTGAGAAACTATAAAA 540
    |||
QY 580 CATTGGTGAATCCAGCAATGTGACTTTAAACCTATGAAGGTATGATGACAGATTGCT 639
    |||
DB 541 CATTGGTGAATCCAGCAATGTGACTTTAAACCTATGAAGGTATGATGACAGATTGCT 600
    |||
QY 640 GTCAACAGGAATGATGATGTCAAGCAATTCATTGATTAACCTCCATCCCAATTGAT 699
    |||
DB 601 GTCAACAGGAATGATGATGTCAAGCAATTCATTGATTAACCTCCATCCCAATTGAT 660
    |||
QY 700 GAGCTCACTA 709
    |||
DB 661 GAGCTCACTA 670
    |||

```

RESULT 3
AAK56267
ID AAK56267 standard; cDNA; 1486 BP.

XX AAK56267;

XX 19-JUL-1999 (first entry)

DE Human lysophospholipase extended NHP encoding cDNA.

KW Human: lysophospholipase; NHP; cell proliferation; arteriosclerosis;
KW atherosclerosis; buritis; cirrhosis; hepatitis; myelofibrosis;
KW mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
KW polycythemia vera; psoriasis; primary thrombocytopenia; cancer;
KW inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;

KW Immune response; ankylosing spondylitis; autoimmune haemolytic anaemia;
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 76..768

FT /tag= a

FT /product= "NHP"

XX W09849319-1.

XX 05-NOV-1998.

XX 29-APR-1998; 98MO-US08782.

XX 12-FEB-1998; 98US-0022940.

XX 29-APR-1997; 97US-0844120.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Murry LE, Shan P;

XX WPI; 1999-326512/27.

XX P-PSDB; AAY09531.

PT New human lysophospholipase (NHP) polypeptides and polynucleotides
PT which identify and encode NHP

XX Claim 7; Fig 2; 66pp; English.

CC The present sequence encodes human lysophospholipase (NHP). The present
CC invention also describes a method for treating or preventing a disorder
CC of cell proliferation (e.g. arteriosclerosis, atherosclerosis, buritis,
CC cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,
CC paroxysmal nocturnal haemoglobinuria, polycythemia vera, psoriasis,
CC primary thrombocytopenia, and cancers), inflammation (e.g. Addison's
CC disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a
CC disorder of the immune response (e.g. AIDS, allergies, ankylosing
CC spondylitis, autoimmune haemolytic anaemia) by administering an
CC antagonist to NHP. NHP proteins, antagonists, antibodies, agonists,
CC complementary sequences or vectors may be administered in combination
CC with other therapeutic agents. Antibodies which specifically bind to
CC NHP may be used for the diagnosis of disorders characterized by
CC expression of NHP or in assays to monitor patients being treated with
CC NHP or agonists. The polynucleotides (PNS) encoding NHP or fragments
CC may be used therapeutically. In one aspect, the complement of the
CC polynucleotides may be used where it would be desirable to block the
CC transcription of the mRNA. Complementary molecules may be used to
CC modulate NHP activity or to achieve regulation of gene activity.
CC Diagnostically, the PNS may be used to detect and quantitate gene
CC expression in biopsied tissues in which expression of NHP may be
CC correlated with disease.

XX Sequence 1486 BP; 418 A; 304 C; 300 G; 459 T; 5 other;

Query Match 88.6%; Score 628.4; DB 20; Length 1486;

Best Local Similarity 91.0%; Pred. No. 2.3e-190;

Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

```

QY 1 GCGGTCGACAGCCCTTTGGGCGCGCGCGCGCGCTTCTTCCCTTGGCGTGG 60
    |||
DB 2 GCGGTCGACAGCCCTTTGGGCGCGCGCGCGCGCGCTTCTTCCCTTGGCGTGG 61
    |||
QY 61 AGCTGAGCGCGTGTATGCGCGCAATTAACATGTCAACCCCGTGCCTATGTCGCG 120
    |||
DB 62 AGCTGAGCGCGTGTATGCGCGCAATTAACATGTCAACCCCGTGCCTATGTCGCG 121
    |||
QY 121 CCGCCCGGAGAGCGCACCGCTGCGCTGATTTCTTGATGATGATGGAGATGCTG 175
    |||
DB 122 CCGCCCGGAGAGCGCACCGCTGCGCTGATTTCTTGATGATGATGGAGATGCTG 181
    |||
QY 176 ----- 175

```


[illegible]

Db	86	ACCTGACGGGGTGTATGTGCGGCATTAACATGTCAACCCCGTGCCTGCACATCGTGGCCG	145
Qy	121	CGGCCCGAAGGCGCACCCGCTGGCGTGAATTTTCCTGCATGGAATTGGAGACTG-----	175
Db	146	CGGCCCGAAGGCGCACCCGCTGGCGTGAATTTTCCTGCATGGAATTGGAGACTGCGGACG	205
Qy	176	-----	175
Db	206	GATGGGCAAGAACCTTTGCGAGTATCAGAAAGTTCCATATCAAAATATATGCCCCGATG	265
Qy	176	-GCCGTGATGGCGCTTTACATTAATAATATGAACGTGGCATGCGCTTCAGATTTGATATA	234
Db	266	CGCCTGTATAGGCGCTGTTCATTAATAATGAACGTGGCTATGCTTCATGATGTTTGATATA	325
Qy	235	TTGGGCTTTACACAGATTCACAGAGAGATGAATCGGATTAACACAGCAGACAGAAATA	294
Db	326	TTGGGCTTTACACAGATTCACAGAGAGATGAATCTGGGATTAACACAGCAGACAGAAATA	385
Qy	295	TAAAGCTTTGATGATCAAGAAGTGAAGAAATGCGATTCCTTCAACAGAAATATTTTGG	354
Db	386	TAAAGCTTTGATGATCAAGAAGTGAAGAAATGCGATTCCTTCAACAGAAATATTTTGG	445
Qy	355	GAGGCTTTTCTAGGAGAGAGCTTTATCTTATATATAGTCCCTTACACACAGCAAGAAC	414
Db	446	GAGGCTTTTCTAGGAGAGAGCTTTATCTTATATATAGTCCCTTACACACAGCAAGAAC	505
Qy	415	TGGCAGGTGTCAGTCACTCACTGATTTCTTGCTTCCACTTGGGANTTCCCTTTCACAGGKC	474
Db	506	TGGCAGGTGTCAGTCACTCACTGATTTCTTGCTTCCACTTGGGANTTCCCTTTCACAGGTC	565
Qy	475	CTATCGGTGTGCTAATAGATATTTCTTATTTCTCCAGTGCACGCGGATGTGACCTT	534
Db	566	CTATCGGTGTGCTAATAGATATTTCTTATTTCTCCAGTGCACGCGGATGTGACCTT	625
Qy	535	TGGTTCCTCTGATGTTTGGTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCAG	594
Db	626	TGGTTCCTCTGATGTTTGGTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCAG	685
Qy	595	CCAATGTACCTTTAAACCTATGAAGGTATGATGACAGTTCGTGTCACAGGAAATGA	654
Db	686	CCAATGTACCTTTAAACCTATGAGAGTATGATGACAGTTCGTGTCACAGGAAATGA	745
Qy	655	TGGATGTCAAGCAATTCATTGATAAACTCCACTCCAAATGATGAGCTGACTA	709
Db	746	TGGATGTCAAGCAATTCATTGATAAACTCCACTCCAAATGATGAGCTGACTA	800
RESULT 6			
ABV25207			
xx	ID	ABV25207 standard; cDNA; 2600 BP.	
xx	AC	ABV25207;	
xx	DT	16-SEP-2002 (first entry)	
xx	DE	Human prostate expression marker cDNA 25198.	
xx	KW	Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker	
xx	KW	pharmacogenomic marker; gene; ss.	
xx	OS	Homo sapiens.	
xx	PN	WO200160860-A2.	
xx	PD	23-AUG-2001.	
xx	PF	20-FEB-2001; 2001WO-US05171.	
xx	PR	17-FEB-2000; 2000US-183319P.	
xx	PR	16-MAR-2000; 2000US-189862P.	
xx	PR	25-MAY-2000; 2000US-207454P.	
xx	PR	09-JUN-2000; 2000US-211314P.	

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 1538 BP; 403 A; 324 C; 351 G; 460 T; 0 other;

Query Match 85.5%; Score 606.4; DB 23; Length 1538;
 Best Local Similarity 90.7%; Pred. No. 2,6e-183;
 Matches 705; Conservative 1; Mismatches 3; Indels 68; Gaps 3;

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QY 1 GCGGCTCGACGCGCTTGGGCGCGCGCGCGCTCTTCTCTTCCGCTGGCGCTGTG 60
    |||
DB 121 GCGGCTCGACGCGCTTGGGCGCGCGCGCGCTCTTCTCTTCCGCTGGCGCTGTG 180
    |||
QY 61 AGCTGAGGCGGTGTATGTGTGGGCAATACATGCAACCGCGCGCGCGCGCGCGCGCG 120
    |||
DB 181 AGCTGAGGCGGTGTATGTGTGGGCAATACATGCAACCGCGCGCGCGCGCGCGCGCG 240
    |||
QY 121 CGGCGCGGAAAGGCGACCGCGCGGTGATTTTCTCGCATGGATTGGAGATCTGG---- 175
    |||
DB 241 CGGCGCGGAAAGGCGACCGCGCGGTGATTTTCTCGCATGGATTGGAGATCTGGGCGACG 300
    |||
QY 176 ----- 175
    |||
DB 301 GATGGGACAGAGCGCTTGCAGGTATCAGAAATTCACATATCAATATATCTGCCCGCATG 360
    |||
QY 176 -GCGCTGTAGGCGCTGTACATTAAATATGACGTGCGCTATCGCTCATGG--TTGATATT 233
    |||
DB 361 CGCGCTGTAGGCGCTGTATCATTAATATGACGTGCGCTATCGCTCATGGTTTATATT 420
    |||
QY 234 ATTGGGCTTTCACACAGATTACAGAGAGATGATCTGGGANTTAAACAGGACAGCAAAAT 293
    |||
DB 421 ATTGGGCTTTCACACAGATTACAGAGAGATGATCTGGGANTTAAACAGGACAGCAAAAT 480
    |||
QY 294 ATAAAGCTTTATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 352
    |||
DB 481 ATAAAGCTTTATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 540
    |||
QY 353 GGGAGGCTTTTCTCAGAGGAGAGCTTTTACTTATATCTGCGCTTACACACAGCAGAA 412
    |||
DB 541 GGGAGGCTTTTCTCAGAGGAGAGCTTTTACTTATATCTGCGCTTACACACAGCAGAA 600
    |||
QY 413 ACTGCGAGGTGTCTACTGCACTGATTTTCTTCTGCTTCCAGTTGGGNTTCTTCCACAGG 472
    |||
DB 601 ACTGCGAGGTGTCTACTGCACTGATTTTCTTCTGCTTCCAGTTGGGNTTCTTCCACAGG 660
    |||
QY 473 KCTATCGGTGCTTAATAGATTAATTTCTATCTCAGTGCACCGGGGATGTGACCC 532
    |||
DB 661 TCTTATCGGTGCTTAATAGATTAATTTCTATCTCAGTGCACCGGGGATGTGACCC 720
    |||
QY 533 TTGCTTCCCGCTGATGTTGGTCTCTTACGGTGGAAAAAACAATTGGTGAATCC 592
    |||
DB 721 TTGCTTCCCGCTGATGTTGGTCTCTTACGGTGGAAAAAACAATTGGTGAATCC 780
    |||
QY 593 AGCCATGTGACCTTTAAACCTATGAGAGGTATGATGACAGCTTGTCTCAACAGAAAT 652
    |||
DB 781 AGCCATGTGACCTTTAAACCTATGAGAGGTATGATGACAGCTTGTCTCAACAGAAAT 840
    |||
QY 653 GATGATGTCAAGCAATTCATTGATTAACCTCTACCTCAATTTGATGAGTCACTA 709
    |||
DB 841 GATGATGTCAAGCAATTCATTGATTAACCTCTACCTCAATTTGATGAGTCACTA 897
    |||

```

RESULT 8
 AAH26336
 ID AAH26336 standard; cDNA: 758 BP.

AC AAH26336;
 DT 02-Oct-2001 (first entry)
 XX
 DE Human brain lysophospholipase cDNA.
 XX

KW Lysophospholipase; human; brain; lysophospholipid; atherosclerosis;
 KW hyperlipidaemia; dysrhythmia; myocardial ischemia; demyelination;
 KW vasotrophic; antiatherosclerotic; antilipemic; neuroprotective;
 KW gene therapy; Lysopla; ss.

OS Homo sapiens.

Key Location/Qualifiers

CD 49..741

FT /*tag= a

FT /note= "the coding region from position 48 to

FT position 741 is specifically claimed in

FT primer_bind complement (49..74)

FT primer_bind 716..741

FT /*tag= c

PD 02-AUG-2001.

PE 28-JAN-2000; 2000WO-US02319.

PR 28-JAN-2000; 2000US-0493601.

PA (REGC) UNIV CALIFORNIA.

PI Dennis EA; Wang A;

DR WPI: 2001-483215/52.

PT P-PSDB; AAB82669.

PT Novel recombinant lysophospholipid-specific human brain

PT lysophospholipase enzyme useful for treating disease states having

PT elevated concentrations of lysophospholipids, such as atherosclerosis,

PT hyperlipidaemia

PS Claim 1; Fig 1; 38pp; English.

XX The present sequence is that of cDNA encoding a recombinant human

XX brain lysophospholipid-specific lysophospholipase (Lysopla, see

XX AAB82669). Human Lysopla is a novel member of the K/L hydrolase

XX family having a catalytic site composed of Ser-119, Asp-174 and

XX His-208. Lysoplas are critical enzymes that act on biological

XX membranes to regulate the multifunctional lysophospholipids;

XX increased levels of lysophospholipids are associated with a host of

XX diseases. The enzyme is widely distributed in almost all tissues,

XX although levels vary. The Lysopla cDNA was obtained by PCR

XX amplification of human brain cDNA using primers (see AAH26337-38)

XX based on human sequences identified by screening with a mouse

XX Lysopla sequence. The PCR product was expressed in Escherichia coli

XX BL21 (DE3) cells using vector pET28a(a). The recombinant Lysopla

XX protein, which included an N-terminal 6His tag and thrombin cleavage

XX site, was recovered on an Ni-NTA column. Kinetic analysis showed

XX that human Lysopla displays apparent co-operativity and surface

XX dilution kinetics. The recombinant Lysopla can be used in the

XX treatment of disease states having elevated concentrations of

XX lysophospholipids, such as atherosclerosis, hyperlipidaemia, lethal

XX dysrhythmia in myocardial ischemia and segmental demyelination of

XX peripheral nerves. The Lysopla may be supplied to the

XX enzyme-deficient patient by infusion or by gene therapy (both

XX claimed). Also claimed is a method of inhibiting human brain

XX Lysopla activity using methyl arachidonyl fluorophosphates.

XX

SO Sequence 758 BP; 186 A; 177 C; 186 G; 209 T; 0 other;

Query Match 84.7%; Score 600.8; DB 22; Length 758;
 Best Local Similarity 90.5%; Pred. No. 1e-181;
 Matches 678; Conservative 1; Mismatches 4; Indels 66; Gaps 1;

QY 27 CGGAGCGCGCGCTCTTCTGCGCTGAGCTGAGCGGTGTGTGCGGCAAT 86
 |||

```

Db      1 CCGGGCCCGGCTTCCTTCCTCCGCTTGAGCTGAGCGGGCTGTATGTCGGCAAT 60
QY      87 AACATGCAACCCGGCTGCCGCCATGTCGCCGCCGCCGGAAGGCCACCGCTGCGGTG 146
Db      61 AACATGCAACCCGGCTGCCGCCATGTCGCCGCCGCCGGAAGGCCACCGCTGCGGTG 120
QY      147 ATTTTCCGATGATGATGGAGATGCTGG----- 175
Db      121 ATTTTCCGATGATGATGGAGATGCTGGAGCAGGATGGAGAGCCCTTTCAGATTC 180
QY      176 -----GCCTGTAGCCCTGTACATTAAT 200
Db      181 AGAGTTCATATCAATATATCTGCCGATCGGCTGTAGGCTGTACATTAAT 240
QY      201 ATGAACGCGGATGCGCTTCATGTTGATATTAATGGGCTTTCACAGATTCACAGAG 260
Db      241 ATGAACGCGGATGCGCTTCATGTTGATATTAATGGGCTTTCACAGATTCACAGAG 300
QY      261 GATGAATCTGGATTAACAGGACAGCAAAATATAAAGCTTTGATGATCAAGAAAGTG 320
Db      301 GATGAATCTGGATTAACAGGACAGCAAAATATAAAGCTTTGATGATCAAGAAAGTG 360
QY      321 AAGAAATGCGATCTCTTCTAACAGATTTTGGAGGCTTTCACAGGAGGAGCTTTA 380
Db      361 AAGAAATGCGATCTCTTCTAACAGATTTTGGAGGCTTTCACAGGAGGAGCTTTA 420
QY      381 TCTTATATACCTGCTTACACAGCAAGAACTGGCAGGCTGCTACGCTCAGTTTC 440
Db      421 TCTTATATACCTGCTTACACAGCAAGAACTGGCAGGCTGCTACGCTCAGTTTC 480
QY      441 TTGCTTCCACTTCGGGNTTCTTCCACAGGKCTATCGGTGTGTATATAGATATTT 500
Db      481 TGGCTTCCACTTCGGGNTTCTTCCACAGGKCTATCGGTGTGTATATAGATATTT 540
QY      501 TCTATTCCTCAGTCCACAGGAGATTTGACCTTTGGTCCCTCATGTTGGTCTCTT 560
Db      541 TCTATTCCTCAGTCCACAGGAGATTTGACCTTTGGTCCCTCATGTTGGTCTCTT 600
QY      561 ACGGTGGAATACTAAACATTTGTAATCCAGCAATGTAGCTTTAAACCTATGAA 620
Db      601 ACGGTGGAATACTAAACATTTGTAATCCAGCAATGTAGCTTTAAACCTATGAA 660
QY      621 GGTATGATGACAGATTCGTGTCAACAGAAATGATGATGTCAAGCAATTCATTA 680
Db      661 GGTATGATGACAGATTCGTGTCAACAGAAATGATGATGTCAAGCAATTCATTA 720
QY      681 CTCCTACCTCCATTTGATGAGCTCATA 709
Db      721 CTCCTACCTCCATTTGATGAGCTCATA 749

```

RESULT 9
AAS56597
ID AAS56597 standard; cDNA: 2417 BP.

AC AAS56597;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA for an ovarian cancer protein #221.
XX
KW Human; ss: ovarian cancer protein; cancer; tumour; ovarian cancer;
XX endometrial cancer; cytostatic.
XX Homo sapiens.
XX OS
XX PN WO200170976-A2.
XX PD 27-SEP-2001.
XX PF 20-MAR-2001; 2001WO-US09062.
XX PR 21-MAR-2000; 2000US-190710P.

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PR      22-JUN-2000; 2000US-213748P.  
PR      19-DEC-2000; 2000US-257276P.  
PA      (CORI-) CORIXA CORP.  
PI      Xu J, Pyle RA, Stolk JA;  
XX      WPI; 2001-607531/69.  
DR      Nucleic acids encoding 222 polypeptides associated with ovarian and  
PT      endometrial cancers, useful for diagnosing, preventing and treating  
PS      cancers -  
PS      Claim 1; Page 186-187; 187pp; English.  
CC      The invention relates to human polynucleotides encoding proteins  
CC      associated with ovarian and endometrial cancers. The polynucleotides and  
CC      the proteins they encode may be used in the prevention, diagnosis and  
CC      treatment of diseases associated with the inappropriate expression of  
CC      ovarian and endometrial cancer polypeptides (OECs). For example, the  
CC      polynucleotide (or an expression vector comprising the polynucleotide)  
CC      and the OEC may be used to treat disorders associated with decreased  
CC      expression by rectifying mutations or deletions in a patient's genome  
CC      that affect the activity of OECs by expressing inactive proteins or to  
CC      supplement the patient's own production of them. Additionally, the  
CC      polynucleotide may be used to produce the OECs, by inserting the protein.  
CC      The acids into a host cell and culturing the cell to express the protein. The  
CC      probes in diagnostic assays to detect and quantitate the presence of  
CC      similar nucleic acids in samples, and therefore which patients may be in  
CC      need of restorative therapy. The OECs may also be used as antigens in  
CC      the production of anti-OEC antibodies and in assays to identify  
CC      modulators of its expression and activity. The anti-OEC antibodies and  
CC      antagonists may also be used to down regulate expression and activity.  
CC      The anti-OEC antibodies may also be used as diagnostic agents for  
CC      detecting the presence of OEC in samples (e.g. by enzyme linked  
CC      immunosorbent assay (ELISA)) and hence diagnose patients with  
CC      cancers. The present sequence is a ovarian and endometrial cancer linked  
CC      cDNA of the invention.  
XX  
SQ      Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 other;  
XX  
Query Match      83.1%; Score 589.4; DB 22; Length 2417;  
Best Local Similarity 90.5%; Pred. No. 9,5e-178;  
Matches 666; Conservative 1; Mismatches 66; Gaps 1;  
QY      40 CTTCCTTCGCTTGGCGTGTAGCTGAGCGCTGTATGTCGGCAATATGTCACACC 99  
Db      1 CTTCCTTCGCTTGGCGTGTAGCTGAGCGCTGTATGTCGGCAATATGTCACACC 60  
QY      100 CGGTGCGCGCATGCTGCGCGCGCGCGGAGGACCGCTGCGGTATTTCTCGCATG 159  
Db      61 CGGTGCGCGCATGCTGCGCGCGCGCGGAGGACCGCGCTGCGGTATTTCTCGCATG 120  
QY      160 GATGCGAGATGCTG----- 175  
Db      121 GATGCGAGATGCTGCGAGCGATGGCAGACCTTTCAGATATCAGAAATTCACATA 180  
QY      176 -----GCCTGTAGCCCTGTACATTAATATGAAAGGCTA 213  
Db      181 TCAATATATCTGCCGATGCGCTGTAGGCTGTACATTAATATGAAAGGCTA 240  
QY      214 TCCCTTATGCTTATATATGATGCTTTCACAGATTCACAGAGGATGATCTGGGA 273  
Db      241 TCCCTTATGCTTATATATGATGCTTTCACAGATTCACAGAGGATGATCTGGGA 300  
QY      274 TTAACAGGACAGAAATATAAAGCTTTGATGATCAAGATGAGATTC 333  
Db      301 TTAACAGGACAGAAATATAAAGCTTTGATGATCAAGATGAGATTC 360  
QY      334 CTTCATACAGATTAATTTGGAGGCTTTCACAGGAGGAGCTTATCTTATATCTG 393  
Db      361 CTTCATACAGATTAATTTGGAGGCTTTCACAGGAGGAGCTTATCTTATATCTG 420

```

CC determining tumor characteristics in a tissue sample taken from a
 CC patient. The present sequence represents a human lipid-associated gene
 CC related cDNA sequence, which is used in the exemplification of the
 CC present invention.

XX Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 other;

Query Match 83.1%; Score 589.4; DB 24; Length 2417;
 Best Local Similarity 90.5%; Pred. No. 9.5e-178;
 Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 394 CCTTACACAGACAGAACTGGCAGGTGCTACGTGCTTCTTCCACTTC 453
 |||||||
 DB 421 CCTTACACAGACAGAACTGGCAGGTGCTACGTGCTTCTTCCACTTC 480
 |||||||
 QY 454 GGGATTCCTTCCACAGGKCTATGCTGCTTAAATAGATATTTCTTCAGT 513
 |||||||
 DB 481 GGGATTCCTTCCACAGGKCTATGCTGCTTAAATAGATATTTCTTCAGT 540
 |||||||
 QY 514 GCCACGGGATGTGACCCCTTGGTCCCTGATGTTGGTCTCTTACGTTGAAAAAC 573
 |||||||
 DB 541 GCCACGGGATGTGACCCCTTGGTCCCTGATGTTGGTCTCTTACGTTGAAAAAC 600
 |||||||
 QY 574 TAAAAACATTGGTGAATCCAGCCCAATGTGACCTTAAAAACCTATGAAGTATGTCACA 633
 |||||||
 DB 601 TAAAAACATTGGTGAATCCAGCCCAATGTGACCTTAAAAACCTATGAAGTATGTCACA 660
 |||||||
 QY 634 GTTCGTGTCAACAGAAATGATGATGTCAGCAATTCATGATTAACCTCTACCTCCAA 693
 |||||||
 DB 661 GTTCGTGTCAACAGAAATGATGATGTCAGCAATTCATGATTAACCTCTACCTCCAA 720
 |||||||
 QY 694 TTGATTGACGTCACTA 709
 |||||||
 DB 721 TTGATTGACGTCACTA 736
 |||||||

RESULT 10
 ID ABL59514
 ID ABL59514 standard; cDNA; 2417 BP.
 XX ABL59514;
 AC
 XX 16-JUL-2002 (first entry)
 DT
 DE Human lysophospholipase cDNA seq ID NO:14.
 XX
 XX Human; lysophospholipase; enzyme; chromosome 8; tumour;
 KW lipid associated gene; lipid metabolism; lipid synthesis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200227028-A1.
 XX
 PD 04-APR-2002.
 XX
 XX 27-SEP-2001; 2001WO-US30366.
 PF
 XX 28-SEP-2000; 2000US-0676052.
 PR
 XX (ATAI-) AITAIRGIN TECHNOLOGIES INC.
 PA
 XX Skinner MK, Patton JL, Chaudhary J;
 PI WPI; 2002-402054/43.
 XX
 DR
 XX
 PT Identifying tumor characteristics in a tissue sample taken from a
 PT patient. Involves determining the copy number or expression level of
 PT genes associated with lipid metabolism, synthesis or action
 XX
 PS Example 1; Page 73; 113pp; English.
 XX
 CC The present invention describes a method for identifying tumour
 CC characteristics, comprising measuring a copy number or expression level
 CC of at least two genes associated with lipid metabolism, synthesis, or
 CC action in cells from a patient tissue sample, and comparing the results
 CC with a copy number or expression level of the genes in a normal cell.
 CC Also described is an array of nucleic acid polymers immobilised on a
 CC solid support, comprising a solid support, at least two different nucleic
 CC acid polymers which are each specific for a different gene associated
 CC with lipid metabolism, synthesis or action, where each nucleic acid
 CC polymer is located at a predetermined position on the solid support, and
 CC the array comprises nucleic acid polymers which are specific for less
 CC than 100 genes other than the selected genes. The method is useful for

CC determining tumor characteristics in a tissue sample taken from a
 CC patient. The present sequence represents a human lipid-associated gene
 CC related cDNA sequence, which is used in the exemplification of the
 CC present invention.

XX Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 other;

Query Match 83.1%; Score 589.4; DB 24; Length 2417;
 Best Local Similarity 90.5%; Pred. No. 9.5e-178;
 Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 40 CTTCCTTCGCTTGGCTGTGAGTGTAGCGGTGTATGTGCGCAATTAATGTCACACC 99
 |||||||
 DB 1 CTTCCTTCGCTTGGCTGTGAGTGTAGCGGTGTATGTGCGCGCAATTAATGTCACACC 60
 |||||||
 QY 100 CGCTGCCCGCCATTCGTCGCCGCCGCCGCCGGAAGCCACCGCTGCGTATTTCCGCAATG 159
 |||||||
 DB 61 CGCTGCCCGCCATTCGTCGCCGCCGCCGCCGGAAGCCACCGCTGCGTATTTCCGCAATG 120
 |||||||
 QY 160 GATTGGAGATPACTGG-----
 |||||||
 DB 121 GATTGGAGATPACTGGGCGAGATGGCGAAGCCTTTGCAAGTATCAGAACTTCACATA 180
 |||||||
 QY 176 -----GCTGTAGGCTGTACATTAAATATGAACGTGCTA 213
 |||||||
 DB 181 TCAATATATCTGCCCGCATGGCCTGTAGGCTGTACATTAAATATGAACGTGCTA 240
 |||||||
 QY 214 TGCCTTCATGCTTATATATATGCGCTTACCCAGATTCACAGAGATGAATCTGGGA 273
 |||||||
 DB 241 TGCCTTCATGCTTATATATATGCGCTTACCCAGATTCACAGAGATGAATCTGGGA 300
 |||||||
 QY 274 TTAACAGGACAGCAAAATATAAAGCTTGTATGATCAATGAAGTAAATGGCATTC 333
 |||||||
 DB 301 TTAACAGGACAGCAAAATATAAAGCTTGTATGATCAATGAAGTAAATGGCATTC 360
 |||||||
 QY 334 CTTCCTTACAGAAATATTTTGGAGGTTTCTCAGAGAGAGCTTATCTTTAATATCTG 393
 |||||||
 DB 361 CTTCCTTACAGAAATATTTTGGAGGTTTCTCAGAGAGAGCTTATCTTTAATATCTG 420
 |||||||
 QY 394 CCTTACACAGACAGAACTGGCAGGTGCTACGTGCTTCTTCCACTTC 453
 |||||||
 DB 421 CCTTACACAGACAGAACTGGCAGGTGCTACGTGCTTCTTCCACTTC 480
 |||||||
 QY 454 GGGATTCCTTCCACAGGKCTATGCTGCTTAAATAGATATTTCTTCAGT 513
 |||||||
 DB 481 GGGATTCCTTCCACAGGKCTATGCTGCTTAAATAGATATTTCTTCAGT 540
 |||||||
 QY 514 GCCACGGGATGTGACCCCTTGGTCCCTGATGTTGGTCTCTTACGTTGAAAAAC 573
 |||||||
 DB 541 GCCACGGGATGTGACCCCTTGGTCCCTGATGTTGGTCTCTTACGTTGAAAAAC 600
 |||||||
 QY 574 TAAAAACATTGGTGAATCCAGCCCAATGTGACCTTAAAAACCTATGAAGTATGTCACA 633
 |||||||
 DB 601 TAAAAACATTGGTGAATCCAGCCCAATGTGACCTTAAAAACCTATGAAGTATGTCACA 660
 |||||||
 QY 634 GTTCGTGTCAACAGAAATGATGATGTCAGCAATTCATGATTAACCTCTACCTCCAA 693
 |||||||
 DB 661 GTTCGTGTCAACAGAAATGATGATGTCAGCAATTCATGATTAACCTCTACCTCCAA 720
 |||||||
 QY 694 TTGATTGACGTCACTA 709
 |||||||
 DB 721 TTGATTGACGTCACTA 736
 |||||||

RESULT 11
 ID ABK37030
 ID ABK37030 standard; cDNA; 2417 BP.
 XX ABK37030;
 AC
 XX 08-MAY-2002 (first entry)
 DT
 XX DNA encoding human lysophospholipase I #1.
 DE

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antilipemic; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy; gene; ss.
 OS Homo sapiens.
 PN WO200210185-A1.
 XX PD 07-FEB-2002.
 XX PF 20-JUL-2001; 2001WO-US22975.
 XX PR 31-JUL-2000; 2000US-0629645.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Bennett CF, Wyatt JR;
 XX DR WPI; 2002-188720/24.
 XX DR P-PSDB; AAU85132.
 XX PT Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX
 XX PS Example 13; Page 88-90; 131pp; English.
 XX CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191
 CC represent lysophospholipase I coding sequences, antisense
 CC oligonucleotides and related PCR primers of the invention.
 CC
 XX SQ Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 other;
 Query Match 83.1%; Score 589.4; DB 24; Length 2417;
 Best Local Similarity 90.5%; Pred. No. 9.5e-178;
 Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;
 QY 40 CTTCCTCCGCTGCTGCTGAGCTGAGCGGCTATGTGCGGCAATACATGTCAACC 99
 Db 1 CTTCCTCCGCTGCTGCTGAGCTGAGCGGCTATGTGCGGCAATACATGTCAACC 60
 QY 100 CGCTGCCCGCATGTGCGCGCGCGCGGAGAGCGCACCGCTGCGGTATTTCTCGATG 159
 Db 61 CGCTGCCCGCATGTGCGCGCGCGCGGAGAGCGCACCGCTGCGGTATTTCTCGATG 120
 QY 160 GATTGGAGATCTAG----- 175
 Db 121 GATTGGAGATCTAGCGGAGCGATGGGAGAGAGCTTTGACAGTATCAGAAAGTTACATA 180
 QY 176 -----GCCTGTAGCGCTGTATACATTAATATGACGTGGCTA 213
 Db 181 TCAATATATCTGCCCGCATGCCCTGTAGGCTGTATACATTAATATGACGTGGCTA 240
 QY 214 TGCCTTATGTTGATTTTGTGGCTTACACAGATTCACAGAGAGATGAAATCTGGGA 273
 Db 241 TGCCTTATGTTGATTTTGTGGCTTACACAGATTCACAGAGAGATGAAATCTGGGA 300
 QY 274 TTAACAGGACAGAAAATATTAAGCTTGATTGATCAAGAGTAAGATGGCATTC 333
 Db 301 TTAACAGGACAGAAAATATTAAGCTTGATTGATCAAGAGTAAGATGGCATTC 360
 QY 334 CTCTAACGAAATATTTTGGAGGCTTCTCAGGGAGAGAGCTTTATCTTTATTAATCTG 393

Db 361 CTCTAACGAAATATTTTGGAGGCTTCTCAGGGAGAGAGCTTTATCTTTATTAATCTG 420
 QY 394 CCCTTACACACAGAAAATCTGCGAGTGTACTGCTACAGTTCTTCTGCTTCCACTTC 453
 Db 421 CCCTTACACACAGAAAATCTGCGAGTGTACTGCTACAGTTCTTCTGCTTCCACTTC 480
 QY 454 GGGNTTCTTCTTCCACAGGAGGCTATCGGGTGTAAATAGAAATATTTCTATTCAGT 513
 Db 481 GGGCTTCTTCTTCCACAGGAGGCTATCGGGTGTAAATAGAAATATTTCTATTCAGT 540
 QY 514 GCCACGGGATTTGACCTTTGTTCCCTGATGTTTGGTTCTTCAAGTGGAAAAAC 573
 Db 541 GCCACGGGATTTGACCTTTGTTCCCTGATGTTTGGTTCTTCAAGTGGAAAAAC 600
 QY 574 TAAACATTTGTTGAATCCAGCCAAATGACCTTTAAACCATAGAAAGTATGATGCA 633
 Db 601 TAAACATTTGTTGAATCCAGCCAAATGACCTTTAAACCATAGAAAGTATGATGCA 660
 QY 634 GTTCGTCAACAGAAATGATGATGTCACCAATTCATTGATTAACCTCTACCTCCAA 693
 Db 661 GTTCGTCAACAGAAATGATGATGTCACCAATTCATTGATTAACCTCTACCTCCAA 720
 QY 694 TTGATTGACGTCACTA 709
 Db 721 TTGATTGACGTCACTA 736

RESULT 12

AAZ61501
ID AAZ61501 standard; cDNA; 1300 BP.XX AAZ61501;
AC 19-UDN-2000 (first entry)

XX DT 19-UDN-2000 (first entry)

XX DE cDNA encoding a human lysophospholipase protein designated CBFLH05.

XX KW Human; lysophospholipase; CBFLH05; liver disease; cancer;
 KW autoimmune disease; kidney disorder; vaccine; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT CDS 6..650
 FT /*tag= a
 FT /product= "lysophospholipase"

XX PN WO200009556-A1.

XX PD 24-FEB-2000.

XX PF 11-AUG-1998; 98WO-CN00164.

XX PR 11-AUG-1998; 98WO-CN00164.

XX PA (UYSH-) UNIV SHANGHAI SECOND MEDICAL.

XX PI Zhou J, Mao M, Ye M, Zhang Q;

XX DR WPI; 2000-224281/19.

XX DR P-PSDB; AAT69296.

XX PT New human lysophospholipase gene (designated CBFLH05) polypeptides and
 PT polynucleotides used to identify agonists, antagonists and inhibitors
 PT for use in (gene) therapy -

XX PS Claim 1; Page 22-23; 36pp; English.

XX CC The present sequence encodes a human lysophospholipase protein
 CC (designated CBFLH05). CBFLH05 polypeptides may be used for
 CC identifying agonists and antagonists/inhibitors, and for detecting
 CC and treating diseases associated with inappropriate CBFLH05 activity

CC or levels. CBRBLH05 polypeptides and polynucleotides, agonists,
 CC antagonists and antibodies are used for the treatment of liver diseases,
 CC cancer, autoimmune diseases, and kidney disorders. The polynucleotide
 CC is also useful as a source of primers and probes, and also for detecting
 CC the above diseases. The polypeptide may also be used as a vaccine.

XX Sequence 1300 BP; 381 A; 246 C; 254 G; 419 T; 0 other;

Query Match 79.1%; Score 561; DB 21; Length 1300;
 Best Local Similarity 92.2%; Pred. No. 8,2e-169;
 Matches 607; Conservative 1; Mismatches 32; Indels 18; Gaps 1;

```

OY 70 GGTGATGCGGCGAATAACATGTCACCCGCGCCGCGCATGTCGCCGCCGCCGCGA 129
    |||||
DB 1 GGTGATGCGGCGAATAACATGTCACCCGCGCCGCGCATGTCGCCGCCGCCGCGA 60
OY 130 AGGCCACGCGTGGGATGATTTCCGTCATGATGAGATGAGATGAGGCTGTAGCCTG 189
    |||||
DB 61 AGGCCACGCGTGGGATGATTTCCGTCATGATGAGATGAGATGAGGCTGTAGCCTG 120
OY 190 TTACATT-----AAATATGAACGTGGCTATGCTTCATGCTTTGATA 231
    |||||
DB 121 AAGCCTTTCAGAGTATCAGAAATTCATCAATATATCTGCCGATCGTTTGATA 180
OY 232 TTATTGGGCTTTCACACAGATTCACAGAGATGATGAGATTAACAGGCGAGAGAA 291
    |||||
DB 181 TTATTGGGCTTTCACACAGATTCACAGAGATGATGAGATTAACAGGCGAGAGAA 240
OY 292 ATATATAAGCTTTGATGATATCAAGAAGTGAAGATGCGATTCCTTTACAGAAATTA 351
    |||||
DB 241 ATATATAAGCTTTGATGATATCAAGAAGTGAAGATGCGATTCCTTTACAGAAATTA 300
OY 352 TGGGAGGCTTTTCAGAGGAGAGCTTATCTTATATACAGCCCTTACACAGAGAGA 411
    |||||
DB 301 TGGGAGGCTTTTCAGAGGAGAGCTTATCTTATATACAGCCCTTACACAGAGAGA 360
OY 412 AACTGGCAGGTGTCACCTCAGTTCCTTGCTTCACCTCGGAGNTTCTTTCCACAGG 471
    |||||
DB 361 AACTGGCAGGTGTCACCTCAGTTCCTTGCTTCACCTCGGAGNTTCTTTCCACAGG 420
OY 472 GKCCTATGGGTGCTAATAGAGATATTTTATTTCTCACTGCCAGGCGGATTTGACC 531
    |||||
DB 421 GTCCTATGGGTGCTAATAGAGATATTTTATTTCTCACTGCCAGGCGGATTTGACC 480
OY 532 CTTTGCTCCCTGATGTTGTTGTTCTTACGTTGAGAAACCTAATAACATTGGTGAATC 591
    |||||
DB 481 CTTTGCTCCCTGATGTTGTTGTTCTTACGTTGAGAAACCTAATAACATTGGTGAATC 540
OY 592 CAGCCAAATGTACCTTTAAACCTATGAAGGTATGATGACAGATTCCTGTCAACAGAAA 651
    |||||
DB 541 CAGCCAAATGTACCTTTAAACCTATGAAGGTATGATGACAGATTCCTGTCAACAGAAA 600
OY 652 TGATGAGATGTACAGCAATTCATGATAACCTCACTCCCAATTGATTGACGTCACTA 709
    |||||
DB 601 TGATGAGATGTACAGCAATTCATGATAACCTCACTCCCAATTGATTGACGTCACTA 658

```

RESULT 13

ID ABR37037 standard; cDNA: 693 BP.

XX ABR37037;

XX 08-MAY-2002 (first entry)

XX DNA encoding mouse lysophospholipase I #1.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antiinflammatory; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy; gene; ss.

OS Mus sp.

```

XX XX
PN W0200210185-A1.
XX XX
PD 07-FEB-2002.
XX XX
PF 20-JUL-2001; 2001WO-US22975.
PR 31-JUL-2000; 2000US-0629645.
XX XX
PA (ISIS-) ISIS PHARM INC.
XX XX
PI Bennett CF, Wyatt JR.
XX XX
DR WPI; 2002-188720/24.
XX XX
PT P-PSDB; AA085133.
XX XX
PS Example 13; Page 92-93; 131pp; English.

```

CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. ABR37028-ABR37191
 CC represent lysophospholipase I coding sequences, antisense
 CC oligonucleotides and related PCR primers of the invention.

XX Sequence 693 BP; 181 A; 168 C; 158 G; 186 T; 0 other;

Query Match 61.5%; Score 436; DB 24; Length 693;
 Best Local Similarity 79.9%; Pred. No. 6.1e-129;
 Matches 554; Conservative 1; Mismatches 72; Indels 66; Gaps 1;

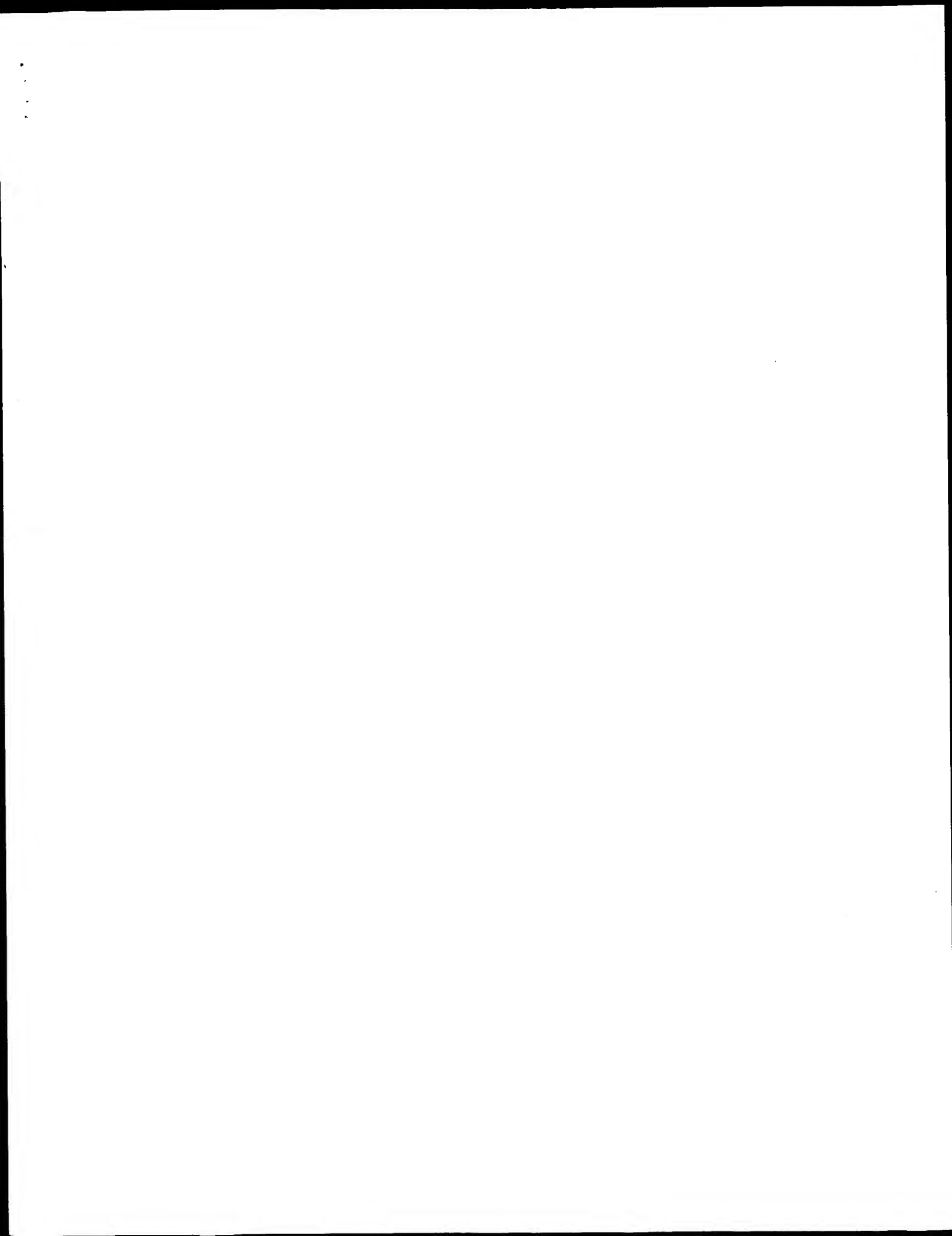
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OY 75 ATGTGGCGCAATTAACATGTCACCCGCGTCCCGCATGTCGCCGCCGCCGGAAGGCC 134
    |||||
DB 1 ATGTGGCGCAATTAACATGTCACCCGCGTCCCGCATGTCGCCGCCGCCGGAAGGCC 60
OY 135 ACCGCTGCGGTGATTTTCTCGCATGATGATGGGATGATGCTGG-----176
    |||||
DB 61 ACCGCTGCGGTGATTTTCTCGCATGATGATGGGATGATGCTGG-----176
OY 177 -----CCTGTTAGGCGT 188
    |||||
DB 121 TTTCGAGGATTCAAAGATCCCAATCAATATACATCTGTCACATGCCCTGTGATGCCA 180
OY 189 GTTACATTAATATGAACGCTGCTATGCTTCAATGTTGATTAATTTGGGCTTTTCACCA 248
    |||||
DB 181 GTTACATTAATATGAACGCTGCTATGCTTCAATGTTGATTAATTTGGGCTTTTCACCA 240
OY 249 GATTCAAGAGATGATGATGATGATTAACAGGACGACGAGAAATATTAAGCTTGGATT 308
    |||||
DB 241 GATTCCAGGAGATGATGATGATGATTAACAGGACGACGAGAAATATTAAGCTTGGATT 300
OY 309 GATCAAGAGATGATGATGATGATGATTAACAGGATTAATTTGGGAGGTTTCTCTCAG 368
    |||||
DB 301 GATCAAGAGATGATGATGATGATGATTAACAGGATTAATTTGGGAGGATTTTCTCTCAG 360
OY 369 GGAGAGCTTATCTTATATATGCTTACACACAGACAGAAATGCGAGGTGCTACT 428
    |||||
DB 361 GGAGAGCTTATCTTATATATGCTTACACACAGACAGAAATGCGAGGTGCTACT 420
OY 429 GCACCTAGTTTCTGCTTCACCTTTCCTTTCCACAGGAGGCTATGCGTGGTCT 488
    |||||
DB 421 GCACCTAGTTTCTGCTTCACCTTTCCTTTCCACAGGAGGCGCATCAACAGTCT 480

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XX (CORI-) CORIXA CORP.
PA
XX
PI Jiang Y, Harlocker SL, Secret H;
XX
DR WPI; 2002-114514/15.
XX
PT Novel isolated colon tumor polynucleotide differentially expressed in
PT colon tumor or colon metastatic tumor and polypeptides encoded by them,
XX useful for inhibiting development of cancer in patient -
XX
PS Claim 1; SEQ ID 1369; 105bp; English.
XX
CC ABL36412 to ABL38645 represent human colon tumor antigen cDNA clones (I)
CC which were isolated from human colon tumour and colon metastatic tumour
CC cDNA libraries. (I) have cytostratic activity and can be used in vaccine
CC production. (I) can be used for stimulating and/or expanding T cells
CC specific for a tumour protein on contact with the T cells. They are also
CC useful for inhibiting the development of cancer in a patient. (I) can be
CC used as probes or primers for nucleic acid hybridisation, for preparing
CC mutant species primers, or primers for use in genetic constructions. (I)
CC can be used in the diagnosis of a colon tumour.
XX
SQ Sequence 419 BP; 125 A; 95 C; 88 G; 109 T; 2 other;
Query Match 55.4%; Score 392.6; DB 24; Length 419;
Best Local Similarity 98.7%; Pred. No. 3.6e-115;
Matches 393; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 312 CAAGAAGTGAAGATGGCTTCCTCTCAACAGATTTATTTGGAGGGTTTCTCAGGGA 371
DB :|||||
DB 417 HAAGAAGTGAAGATGGCTTCCTCTCAACAGATTTATTTGGAGGGTTTCTCAGGGA 358
OY 372 GGAGCTTTATCTTTATATCTGCTTCCACACAGCAAGCAAGCAAGTGGTCTACTGCA 431
DB :|||||
DB 357 GGAGCTTTATCTTTATATCTGCTTCCACACAGCAAGCAAGTGGTCTACTGCA 298
OY 432 CTCAGTTCTGCTTCCACTTGGGNTTCTTCCACAGGKCTATCGTGTCTAAT 491
DB :|||||
DB 297 CTCAGTTCTGCTTCCACTTGGGNTTCTTCCACAGGKCTATCGTGTCTAAT 238
OY 492 AAGATATTTCTATCTCAGTGCACGGGATGTGAACCTTTGGTCCCTGATGTTT 551
DB :|||||
DB 237 AAGATATTTCTATCTCAGTGCACGGGATGTGAACCTTTGGTCCCTGATGTTT 178
OY 552 GGTTCTTAGGGTGAAGAACTAATAACATGSGATCCAGCAATGTGACCTTAA 611
DB :|||||
DB 177 GGTTCTTAGGGTGAAGAACTAATAACATGSGATCCAGCAATGTGACCTTAA 118
OY 612 ACCATGAAGTATGATGACATGCTGTCACAGAAATGATGATGTCAAGCAATTC 671
DB :|||||
DB 117 ACCATGAAGTATGATGACATGCTGTCACAGAAATGATGATGTCAAGCAATTC 58
OY 672 ATTGATTAACCTCTACCTCCATTTGATGACGTCACTA 709
DB :|||||
DB 57 ATTGATTAACCTCTACCTCCATTTGATGACGTCACTA 20

Search completed: January 19, 2003, 01:43:02
Job time : 307 secs



[illegible]

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QY 61 AGCTGAGCGGCTGTATGTGCGCAATACATGTCAACCCCGCTGCCCGCATCTGCCCG 120
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Db 61 AGCTGAGCGGCTGTATGTGCGCAATACATGTCAACCCCGCTGCCCGCATCTGCCCG 120
QY 121 CCGCCCGGGAAGGCGACCGCTGGCGGTATTTCTCGCATGAGTGGAGATCTAGCGCGCTG 180
    |||||||
Db 121 CCGCCCGGGAAGGCGACCGCTGGCGGTATTTCTCGCATGAGTGGAGATCTAGCGCGCTG 180
QY 181 TTAGGCGCTTTACATTAATATGAAAGTGGCTATGCGCTTCATGTTTGTATTTATTTGGG 240
    |||||||
Db 181 TTAGGCGCTTTACATTAATATGAAAGTGGCTATGCGCTTCATGTTTGTATTTATTTGGG 240
QY 241 TTTCACCAATTCACAGGAGGAGTATGCGGATTAACAGGACAGAGAAATATTAAGAAG 300
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Db 241 TTTCACCAATTCACAGGAGGAGTATGCGGATTAACAGGACAGAGAAATATTAAGAAG 300
QY 301 CTTTGATGATCAAGAGGAGGAGTATGCGGATTAACAGGAGTATTTTGGAGGCT 360
    |||||||
Db 301 CTTTGATGATCAAGAGGAGGAGTATGCGGATTAACAGGAGTATTTTGGAGGCT 360
QY 361 TTTCAGGAGGAGGAGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 420
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Db 361 TTTCAGGAGGAGGAGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 420
QY 421 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGCTATG 480
    |||||||
Db 421 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGCTATG 480
QY 481 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGCTATG 540
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Db 481 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGCTATG 540
QY 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTTAAACATTTGGTGAATCCAGCCATG 600
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Db 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTTAAACATTTGGTGAATCCAGCCATG 600
QY 601 TGACCTTTAAACCTATGAAGTATGATGACAGCTTCGATGCAAGGAGGAGGAGGAGGAG 660
    |||||||
Db 601 TGACCTTTAAACCTATGAAGTATGATGACAGCTTCGATGCAAGGAGGAGGAGGAGGAG 660
QY 661 TCAAGCAATTCATGATTAACCTCTACCTCCATTCATGATGAGCTGACTA 709
    |||||||
Db 661 TCAAGCAATTCATGATTAACCTCTACCTCCATTCATGATGAGCTGACTA 709

RESULT 2
US-09-022-940-2
; Sequence 2, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-022-940-2

Query Match      99.8%; Score 707.6; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 4, 3e-226;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTGCGACGCCCTTGGCGCGCGCGCGCGCGCTTCCCTCCGCTGCGCTGTG 60
    |||||||
Db 1 GCCGCTGCGACGCCCTTGGCGCGCGCGCGCGCGCGCTTCCCTCCGCTGCGCTGTG 60
QY 61 AGCTGAGCGGCTGTATGTGCGCAATAATGTCACCCCGCTGCCCATGCTGCCCG 120
    |||||||
Db 61 AGCTGAGCGGCTGTATGTGCGCAATAATGTCACCCCGCTGCCCATGCTGCCCG 120
QY 121 CCGCCCGGGAAGGCGACCGCTGGCGGTATTTCTCGCATGAGTGGAGATCTAGCGCGCTG 180
    |||||||
Db 121 CCGCCCGGGAAGGCGACCGCTGGCGGTATTTCTCGCATGAGTGGAGATCTAGCGCGCTG 180
QY 181 TTAGGCGCTTTACATTAATATGAAAGTGGCTATGCGCTTCATGTTTGTATTTATTTGGG 240
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Db 181 TTAGGCGCTTTACATTAATATGAAAGTGGCTATGCGCTTCATGTTTGTATTTATTTGGG 240
QY 241 TTTCACCAATTCACAGGAGGAGTATGCGGATTAACAGGACAGAGAAATATTAAGAAG 300
    |||||||
Db 241 TTTCACCAATTCACAGGAGGAGTATGCGGATTAACAGGACAGAGAAATATTAAGAAG 300
QY 301 CTTTGATGATCAAGAGGAGGAGTATGCGGATTAACAGGAGTATTTTGGAGGCT 360
    |||||||
Db 301 CTTTGATGATCAAGAGGAGGAGTATGCGGATTAACAGGAGTATTTTGGAGGCT 360
QY 361 TTTCAGGAGGAGGAGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 420
    |||||||
Db 361 TTTCAGGAGGAGGAGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 420
QY 421 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGAGGAGGAG 480
    |||||||
Db 421 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGAGGAGGAG 480
QY 481 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGAGGAGGAG 540
    |||||||
Db 481 GTGTCACTGACACGCTTTCTGCTTCCACTTGGGNTTCTTCCACAGGAGGAGGAGGAGGAG 540
QY 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTTAAACATTTGGTGAATCCAGCCATG 600
    |||||||
Db 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTTAAACATTTGGTGAATCCAGCCATG 600
QY 601 TGACCTTTAAACCTATGAAGTATGATGACAGCTTCGATGCAAGGAGGAGGAGGAGGAGGAG 660
    |||||||
Db 601 TGACCTTTAAACCTATGAAGTATGATGACAGCTTCGATGCAAGGAGGAGGAGGAGGAGGAG 660
QY 661 TCAAGCAATTCATGATTAACCTCTACCTCCATTCATGATGAGCTGACTA 709
    |||||||
Db 661 TCAAGCAATTCATGATTAACCTCTACCTCCATTCATGATGAGCTGACTA 709

RESULT 3
US-09-216-386-2
; Sequence 2, Application US/09216386
; Patent No. 6093561

```

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-2

Query Match 99.8%; Score 707.6; DB 3; Length 709;
Best Local Similarity 100.0%; Pred. No. 4.3e-226;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTCGACGCGCTTGGGCGCGGCGCGCGCGCTTCCCTCGCTGGCGTGTG 60
DB 1 GCCGCTCGACGCGCTTGGGCGCGGCGCGCGCGCTTCCCTCGCTGGCGTGTG 60
QY 61 AGCTGAGCGGTGTATGTGCGGCAATACATGTCACCCGCTGCCGATCGTCCG 120
DB 61 AGCTGAGCGGTGTATGTGCGGCAATACATGTCACCCGCTGCCGATCGTCCG 120
QY 121 CCGCGCGAAGGCGCGCTGCGGTGATTTCTTCATGATGTTGGGATGCTGGCGTG 180
DB 121 CCGCGCGAAGGCGCGCTGCGGTGATTTCTTCATGATGTTGGGATGCTGGCGTG 180
QY 181 TTAGGCGCTGTACATTAATATGAACGTGGCTATGCTTCATGTTGATTTTGGGC 240
DB 181 TTAGGCGCTGTACATTAATATGAACGTGGCTATGCTTCATGTTGATTTTGGGC 240
QY 241 TTTCACCAAGATTCACAGAGAGATTAATCTGGGATTAACAGGCGAGAAATATAAG 300
DB 241 TTTCACCAAGATTCACAGAGAGATTAATCTGGGATTAACAGGCGAGAAATATAAG 300
QY 301 CTTTGATGATCAGAAGTGAAGATGSCATTCCTCTCAACAGATTAATTTGGAGGCT 360
DB 301 CTTTGATGATCAGAAGTGAAGATGSCATTCCTCTCAACAGATTAATTTGGAGGCT 360
QY 361 TTCTCAGAGGAGAGCTTTATCTTATATCTGCTTACACACAGACAGAAATGCGAG 420
DB 361 TTCTCAGAGGAGAGCTTTATCTTATATCTGCTTACACACAGACAGAAATGCGAG 420
QY 421 GTGTCATGCGACTGATTTCTTCTGCTTCACCTGGGATTCCTTCCACAGGCKCTATCG 480
DB 421 GTGTCATGCGACTGATTTCTTCTGCTTCACCTGGGATTCCTTCCACAGGCKCTATCG 480

DB 421 GTGTCATGCGACTGATTTCTTCTGCTTCACCTGGGATTCCTTCCACAGGCKCTATCG 480
QY 481 GTGTCATGATAGAGATTTCTATTTCTCCAGTGCACGCGGATGTGACCTTTGGTTC 540
DB 481 GTGTCATGATAGAGATTTCTATTTCTCCAGTGCACGCGGATGTGACCTTTGGTTC 540
QY 541 CCCGTGATGTTGGTTCCTTACGGTGGAAAAACATTAACATTTGGTGAATCCAGCCCATG 600
DB 541 CCCGTGATGTTGGTTCCTTACGGTGGAAAAACATTAACATTTGGTGAATCCAGCCCATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGATGCAAGTTCTGTCTCAACAGAAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAGATGATGATGCAAGTTCTGTCTCAACAGAAATGATGATG 660
QY 661 TCAAGCAATTCATGATTAACCTCTTACCTCCATTTGATTAGCTACTA 709
DB 661 TCAAGCAATTCATGATTAACCTCTTACCTCCATTTGATTAGCTACTA 709

RESULT 4

US-09-213-394-2
Sequence 2, Application US/09213394
Patent No. 6319701

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,394
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOT19
CLONE: 2676650
US-09-213-394-2

Query Match 99.8%; Score 707.6; DB 4; Length 709;
Best Local Similarity 100.0%; Pred. No. 4.3e-226;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTCGACGCGCTTGGGCGCGGCGCGCGCGCTTCCCTCGCTGGCGTGTG 60
DB 1 GCCGCTCGACGCGCTTGGGCGCGGCGCGCGCGCGCTTCCCTCGCTGGCGTGTG 60

QY 61 ACCTGAGGCGGTATGTGCGCAATTAACATGTCAACCCCGCTGCCCGCATCGTCCG 120
 DB 61 ACCTGAGGCGGTATGTGCGCAATTAACATGTCAACCCCGCTGCCCGCATCGTCCG 120
 QY 121 CGGCGCGGAAAGCCACCGCTGGGTGATTTTCCATGATGAATGGAGATCTGGGCTG 180
 DB 121 CGGCGCGGAAAGCCACCGCTGGGTGATTTTCCATGATGAATGGAGATCTGGGCTG 180
 QY 181 TTAGGCTCTGTACATTAATATGAAGTGGCTTCCATGATGAATGGAGATCTGGGCTG 240
 DB 181 TTAGGCTCTGTACATTAATATGAAGTGGCTTCCATGATGAATGGAGATCTGGGCTG 240
 QY 241 TTTCACAGATTCACAGAGAGATGATCTGGATTAACAGGACACAGAAATATTAAG 300
 DB 241 TTTCACAGATTCACAGAGAGATGATCTGGATTAACAGGACACAGAAATATTAAG 300
 QY 301 CTTTGTATGATACAGAGAGATGATCTGGATTAACAGGATTTATTTGGGAGGT 360
 DB 301 CTTTGTATGATACAGAGAGATGATCTGGATTAACAGGATTTATTTGGGAGGT 360
 QY 361 TTTCACAGAGAGATGATCTGGATTAACAGGATTTATTTGGGAGGT 420
 DB 361 TTTCACAGAGAGATGATCTGGATTAACAGGATTTATTTGGGAGGT 420
 QY 421 GTGTCTGCTGCTGATTTCTGCTCCATCTGGGATTTCTTCCACAGGKCTATCG 480
 DB 421 GTGTCTGCTGCTGATTTCTGCTCCATCTGGGATTTCTTCCACAGGKCTATCG 480
 QY 481 GTGTCTGCTGCTGATTTCTGCTCCATCTGGGATTTCTTCCACAGGKCTATCG 540
 DB 481 GTGTCTGCTGCTGATTTCTGCTCCATCTGGGATTTCTTCCACAGGKCTATCG 540
 QY 541 CCTGTATGTTGGTCTCTTACGCTGGAAGAACTAAACATTTGGATTCAGGCATG 600
 DB 541 CCTGTATGTTGGTCTCTTACGCTGGAAGAACTAAACATTTGGATTCAGGCATG 600
 QY 601 TGACCTTTAAACCTATGAAGATGATGATGATGATGATGATGATGATGATGATG 660
 DB 601 TGACCTTTAAACCTATGAAGATGATGATGATGATGATGATGATGATGATGATG 660
 QY 661 TCAAGCAATTCATGATTAACCTTCACTCCATGATGATGATGATGATGATGATG 709
 DB 661 TCAAGCAATTCATGATTAACCTTCACTCCATGATGATGATGATGATGATGATG 709
 RESULT 5
 US-09-022-940-4
 / Sequence 4, Application US/09022940
 / Patent No. 5965423
 / GENERAL INFORMATION:
 / APPLICANT: Hillman, Jennifer L.
 / APPLICANT: Murry, Lynn E.
 / APPLICANT: Shah, Purvi
 / TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
 / NUMBER OF SEQUENCES: 5
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Incyte Pharmaceuticals, Inc.
 / STREET: 3174 Porter Dr.
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/022,940
 / FILING DATE: Filed Herewith
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ. ID NO. 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1486 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-022-940-4
 Query Match 88.6%; Score 628.4; DB 2; Length 1486;
 Best Local Similarity 91.0%; Pred. No. 1,9e-199;
 Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;
 QY 1 GCGCTGCGACAGCCCTTGGGCGGCGGCGGCGGCGGCTCTTCCCTTCCGCTGCTG 60
 DB 2 GCGCTGCGACAGCCCTTGGGCGGCGGCGGCGGCGGCGGCTCTTCCCTTCCGCTG 61
 QY 61 AGCTGAGGCGGTATGTGCGCAATTAATGATCAACCCCGCTGCCCGCATCGTCCG 120
 DB 62 AGCTGAGGCGGTATGTGCGCAATTAATGATCAACCCCGCTGCCCGCATCGTCCG 121
 QY 121 CGGCGCGGAAAGCCACCGCTGCGGTGATTTTCCGATGATGATGATGATGATGATG 175
 DB 122 CGGCGCGGAAAGCCACCGCTGCGGTGATTTTCCGATGATGATGATGATGATGATG 181
 QY 176 ----- 175
 DB 182 GATGGGCAAGAGCCCTTGGCAAGTATCAAGATTCATCAATATATATCTGCCCGATG 241
 QY 176 -GCTGTATAGCCCTGTTACATTAATTAATGAACGTGCTATGCTTATGCTTATGATTTA 234
 DB 242 CGCCTGTATAGCCCTGTTACATTAATTAATGAACGTGCTATGCTTATGCTTATGATTTA 301
 QY 245 TTGGGCTTTCACAGATTCACAGAGATGATGATGATGATGATGATGATGATGATGATG 294
 DB 302 TTGGGCTTTCACAGATTCACAGAGATGATGATGATGATGATGATGATGATGATGATG 361
 QY 295 TAAAGCTTTGATGATCAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 354
 DB 362 TAAAGCTTTGATGATCAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 421
 QY 355 GAGGCTTTTCACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 414
 DB 422 GAGGCTTTTCACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 481
 QY 415 TGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474
 DB 482 TGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
 QY 475 CTATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 534
 DB 542 CTATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
 QY 535 TGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
 DB 602 TGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
 QY 595 CCAATGTGACCTTTAAACCTATGAAGATGATGATGATGATGATGATGATGATGATGATG 654
 DB 662 CCAATGTGACCTTTAAACCTATGAAGATGATGATGATGATGATGATGATGATGATGATG 721
 QY 655 TGGATGTGAAGCAATTCATGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
 DB 722 TGGATGTGAAGCAATTCATGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
 RESULT 6

US-09-216-386-4
; Sequence 4, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1486 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-216-386-4

Query Match 88.6%; Score 628.4; DB 3; Length 1486;
Best Local Similarity 91.0%; Pred. No. 1.9e-199;
Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 1 GCCGCTGCACGCGCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
DB 2 GCCGCTGCACGCGCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 61
QY 61 ACCTAGGCGGTGTATGTGCGCAATAATCATGTCAACCCGCTGCGCCATCTGCCCC 120
DB 62 ACCTAGGCGGTGTATGTGCGCAATAATCATGTCAACCCGCTGCGCCATCTGCCCC 121
QY 121 CGGCCGGAAGGCGACCGGTGCGGTATTTCCCTGATGATTTGGGAGATCTGG----- 175
DB 122 CGGCCGGAAGGCGACCGGTGCGGTATTTCCCTGATGATTTGGGAGATCTGGGCGACG 181
QY 176 ----- 175
DB 182 GATGGGCAAGAGCCTTGGCAGGTATCAGAGTTCATCATATATATATCTGCCCGCATG 241
QY 176 -GCCGTGAGGCGCTTACATTAATATGAACGTGGCTATGCTTCAATGTTTATATA 234
DB 242 CCGCGTTAGGCGCTTACATTAATATGAACGTGGCTATGCTTCAATGTTTATATA 301
QY 235 TTGGGCTTTCACCATTCACAGAGATGATCTGGGATTAAACAGCAGCAGAAATA 294
DB 302 TTGGGCTTTCACCATTCACAGAGATGATCTGGGATTAAACAGCAGCAGAAATA 361
QY 295 TAAAGCTTTGATGATCAAGAAGTGAAGATGSCATCTCTTCAACGAATTTATTTGG 354
DB 362 TAAAGCTTTGATGATCAAGAAGTGAAGATGSCATCTCTTCAACGAATTTATTTGG 421

QY 355 GAGGTTTTCTCAGAGGAGAGAGCTTTATCTTATATACGTGCGCTTACACAGCAGAAAC 414
DB 422 GAGGTTTTCTCAGAGGAGAGAGCTTTATCTTATATACGTGCGCTTACACAGCAGAAAC 481
QY 415 TGGCAGGTGTACATGCACATCAGTTTCTGCTTCCACTGGGGTTCTCTTCCACAGGKAC 474
DB 482 TGGCAGGTGTACATGCACATCAGTTTCTGCTTCCACTGGGGTTCTCTTCCACAGGKAC 541
QY 475 CTATCGGTGTCTTAATAGATATTTCTATCTCCAGTGCACGCGGGAGTTGACCGCTT 534
DB 542 CTATCGGTGTCTTAATAGATATTTCTATCTCCAGTGCACGCGGGAGTTGACCGCTT 601
QY 535 TGGTCCCTGATGTGTGTTCTTACGCGTGGAAAACTAAACATTTGGTGAATCCAG 594
DB 602 TGGTCCCTGATGTGTGTTCTTACGCGTGGAAAACTAAACATTTGGTGAATCCAG 661
QY 595 CCAATGTGACCTTTAAACCTATGAAGTATGATGCACAGTGTGTCAACAGGAATGA 654
DB 662 CCAATGTGACCTTTAAACCTATGAAGTATGATGCACAGTGTGTCAACAGGAATGA 721
QY 655 TGGATGTCAAGCAATTTATGATTAACCTCTACTCCATTTGATGACCTCACTA 709
DB 722 TGGATGTCAAGCAATTTATGATTAACCTCTACTCCATTTGATGACCTCACTA 776

RESULT 7
US-09-629-645A-18
; Sequence 18, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 18
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (195)...(887)
; US-09-629-645A-18

Query Match 88.6%; Score 628.4; DB 4; Length 1556;
Best Local Similarity 91.0%; Pred. No. 1.9e-199;
Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 1 GCCGCTGCACGCGCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
DB 121 GCCGCTGCACGCGCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 180
QY 61 AGCTGAGGCGGTGTATGTGCGCAATAATCATGTCAACCCGCTGCGCCATCTGCCCC 120
DB 181 AGCTGAGGCGGTGTATGTGCGCAATAATCATGTCAACCCGCTGCGCCATCTGCCCC 240
QY 121 CGGCCGGAAGGCGACCGGTGCGGTATTTCCCTGATGATTTGGGAGATCTGG----- 175
DB 241 CGGCCGGAAGGCGACCGGTGCGGTATTTCCCTGATGATTTGGGAGATCTGGGCGACG 300
QY 176 ----- 175
DB 301 GATGGGCAAGAGCCTTGGCAGGTATCAGAGTTCATCATATATATATCTGCCCGCATG 360
QY 176 -GCCGTGAGGCGCTTACATTAATATGAACGTGGCTATGCTTCAATGTTTATATA 234
DB 361 CGCCTGTTAGGCGCTTACATTAATATGAACGTGGCTATGCTTCAATGTTTATATA 420
QY 235 TTGGGCTTTCACCATTCACAGAGATGATCTGGGATTAAACAGCAGCAGAAATA 294
DB 362 TAAAGCTTTGATGATCAAGAAGTGAAGATGSCATCTCTTCAACGAATTTATTTGG 421

Db 421 TTGGGCTTTCACAGATTTCACAGAGGATGATCTGGATTAAACAGGACGAGAAAATA 480
 QY 295 TAAAGCTTTGATTGATCAAGAGTGAAGATGGCATTCCTCTTAACAGAAATTTTGG 354
 Db 481 TAAAGCTTTGATTGATCAAGAGTGAAGATGGCATTCCTCTTAACAGAAATTTTGG 540
 QY 355 GAGGCTTTTCAGAGGAGGAGCTTTATCTTATATACCTGGCTTACACAGACAGAAAC 414
 Db 541 GAGGCTTTTCAGAGGAGGAGCTTTATCTTATATACCTGGCTTACACAGACAGAAAC 600
 QY 415 TGGCAGGTGTCAGTGCACCTAGTTCTGCTCCACTTGGGNTCCCTTTCACAGAGGKC 474
 Db 601 TGGGAGGTGTCAGTGCACCTAGTTCTGCTCCACTTGGGNTCCCTTTCACAGAGGKC 660
 QY 475 CTATCGGTGGTGAATAGAGATATTTCTATCTCCAGTCCAGGGGAGATGGACCCCT 534
 Db 661 CTATCGGTGGTGAATAGAGATATTTCTATCTCCAGTCCAGGGGAGATGGACCCCT 720
 QY 535 TGGTTCCTTGATGTTTGGTCTCTTACGGTGGAAAACTTAAACATTTGGTGAATCCAG 594
 Db 721 TGGTTCCTTGATGTTTGGTCTCTTACGGTGGAAAACTTAAACATTTGGTGAATCCAG 780
 QY 595 CCAATGTGACCTTTAAACCTATGAGAGATGATGACAGCTTGTCTCAACAGAAATGA 654
 Db 781 CCAATGTGACCTTTAAACCTATGAGAGATGATGACAGCTTGTCTCAACAGAAATGA 840
 QY 655 TGGATGTCAGCAATTCATGATTAACCTCTACTCCCAATTTGATGACGTCACCTA 709
 Db 841 TGGATGTCAGCAATTCATGATTAACCTCTACTCCCAATTTGATGACGTCACCTA 895

RESULT 8

US-09-629-645A-3
 ; Sequence 3, Application US/09629645A
 ; Patent No. 6365354
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
 ; FILE REFERENCE: RTS-0137
 ; CURRENT APPLICATION NUMBER: US/09/629,645A
 ; CURRENT FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 164
 ; SEQ ID NO 3
 ; LENGTH: 2417
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (36)...(728)
 US-09-629-645A-3

Query Match

Best Local Similarity 83.1%; Score 589.4; DB 4; Length 2417;
 Best Local Similarity 90.5%; Pred. No. 2.7e-186;
 Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 40 CTTCCTTCGCGCTTGGCGTGTGAGCTGAGCGGCGGTGTGTGCGGCAATTAACATGCAACC 99
 Db 1 CTTCCTTCGCGCTTGGCGTGTGAGCTGAGCGGCGGTGTGTGCGGCAATTAACATGCAACC 60
 QY 100 CGCTGCCCGGCATCGTCCCGCGCGCGGGAAGGCCACCGCTGGCGTATTTTCCTGCATG 159
 Db 61 CGCTGCCCGGCATCGTCCCGCGCGCGGGAAGGCCACCGCTGGCGTATTTTCCTGCATG 120
 QY 160 GATTGGAGATCTGCG----- 175
 Db 121 GATTGGAGATCTGCGAGCAGATGGCAGAAAGCCCTTTCAGAGTATCAGAAATTCACATA 180
 QY 176 -----GCGTTTAAAGCGCTTAAATTAATTAAGCGGCTA 213
 Db 181 TCAAAATATATCTGCCGCGATGCCCTGTATAGGCTGTATCAATTAATTAAGCGGCTA 240
 QY 214 TGCCTTCATGTTTGAATATATATGAGCTTTCACAGATTCACAGAGATGATCGTGGGA 273

Db 241 TGCCTTCATGTTTGAATATATATGAGCTTTCACAGATTCACAGAGATGATCTGGGA 300
 QY 274 TTAACAGGCGACAGAAAATATTAAGCTTTGATGATCAAGAGTGAAGATGCAATTC 333
 Db 301 TTAACAGGCGACAGAAAATATTAAGCTTTGATGATCAAGAGTGAAGATGCAATTC 360
 QY 334 CTTCATACAGAAATTTTGGAGGTTTTCACAGGAGGAGCTTATCTTATATAGTG 393
 Db 361 CTTCATACAGAAATTTTGGAGGTTTTCACAGGAGGAGCTTATCTTATATAGTG 420
 QY 394 CCCTTACACAGAGAAAATCGCAGGTGTCATCGCATGCACTAGTTCTTGGTCCACTTC 453
 Db 421 CCCTTACACAGAGAAAATCGCAGGTGTCATCGCATGCACTAGTTCTTGGTCCACTTC 480
 QY 454 GGGATTCCTTTCACAGAGGKCTATCGGTGGTGTCTAATAGAGATATTTCTATCTCCAGT 513
 Db 481 GGGATTCCTTTCACAGAGGKCTATCGGTGGTGTCTAATAGAGATATTTCTATCTCCAGT 540
 QY 514 GGCAGGGGATGTGACCCCTTGTCCCTGATGTTGTTGTTCTTACGGTGGAAAAAC 573
 Db 541 GGCAGGGGATGTGACCCCTTGTCCCTGATGTTGTTGTTCTTACGGTGGAAAAAC 600
 QY 574 TAAACATTTGTTGATTCACGCAATGTGACCTTTAAACCTATGAGATGATGACACA 633
 Db 601 TAAACATTTGTTGATTCACGCAATGTGACCTTTAAACCTATGAGATGATGACACA 660
 QY 634 GTTCGTGTACAGAGAAATGATGATGTCACAACTTATGATTAACCTCTACTCCAA 693
 Db 661 GTTCGTGTACAGAGAAATGATGATGTCACAACTTATGATTAACCTCTACTCCAA 720
 QY 694 TTGATTGACGTCACTA 709
 Db 721 TTGATTGACGTCACTA 736

RESULT 9

US-09-629-645A-10
 ; Sequence 10, Application US/09629645A
 ; Patent No. 6365354
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
 ; FILE REFERENCE: RTS-0137
 ; CURRENT APPLICATION NUMBER: US/09/629,645A
 ; CURRENT FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 164
 ; SEQ ID NO 10
 ; LENGTH: 693
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(693)
 US-09-629-645A-10

Query Match

Best Local Similarity 61.5%; Score 436; DB 4; Length 693;
 Best Local Similarity 79.9%; Pred. No. 1.8e-135;
 Matches 554; Conservative 1; Mismatches 72; Indels 66; Gaps 1;

QY 75 ATGTGCGCAATTAACATGCAACCGCGTGGCGGCGCATCGCCGCGCGGGAAGGCC 134
 Db 1 ATGTGCGCAACACATATCCGCTCCGATGCCCGCGCTTGTGCGCGCGGGAAGGCC 60
 QY 135 ACCGCTGCGGTGATTTTCTCATGATGATTTGGAGATACCTGGG----- 176
 Db 61 ACCGCGCGGTTATTTCTTCACGAGATGGAGATACAGGGCAGATGAGTGGAGAACGCC 120
 QY 177 -----CTGTTAGGCTT 188
 Db 121 TTTCAGGATACAAAGTCCCGACATCAAAATACATCTGTCCACATGCGCCCTGTGATGCCA 180

Query Match	61.1%;	Score 433.2;	DB 4;	Length 727;
Best Local Similarity	79.1%;	Pred. No. 1.6e-134;		
Matches 553;	Conservative 1;	Mismatches 79;	Indels 66;	Gaps 1

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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0470 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLANOTO2
CLONE: 2768301
US-09-013-881-15

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Query Match      30.6%; Score 217.2; DB 3; Length 1624;
Best Local Similarity 64.9%; Pred. No. 3,4e-62;
Matches 337; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

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QY 173 TGGCCCTTTAGGCTTACATTAATATGACCTGGCTTACCTTATGTTGATAT 232
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 286 TGGCCCTTAGAGTCTGTCACCTCAACATGAAGTGTGATGCTGCTGTTGACT 345
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 233 TATTGGGCTTACCATTCACAGAGAGATGATCTGGATTTAAACAGCAGAGAAA 292
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 346 GATGGGGCTGAGTCCAGATGCCCGCAGAGAGAGAGCTGCAATCAAGAGAGAGAAA 405
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 293 TATAAAAGCTTGTATGATCAAGAGAGAGATGATGCAATTCCTTTAAACAGATTTAT 352
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 406 CATCAAGGCTTATGATGACATGAATGAAGAACGAGATCCCTGCAATGCAATGCTCT 465
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 353 GGGAGGCTTTTCAGAGGAGAGGCTTATCTTATATCTGCTTACACACAGAGAA 412
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 466 GGGAGGCTTTTCAGAGGAGAGGCTTATCTTATATCTGCTTACACACAGAGAA 525
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 413 ACTGGAGGTGTACACTGACTGCTTCTGCTTCCACTTGGGNTTCTTTCACAGAGG 472
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 526 TCTGGCTGCAATCGTGGCTTGAAGCTGCTGCTGCTGCAACGGGGCTTCCCCAGGC 585
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 473 KCCATCGGTGTCTAATAGATATTTCTATTCTCCAGTCCACGGGGATTTGACCC 532
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 586 ACCTATATGCACTGCCAA---GGACCTGGCCATACCTCCAGTGGAGACTGGACCC 642
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 533 TTTTGTTCCCGATGTTGTTGTTCTTCAAGGTGAAAAAATAAAGATGGATATCC 592
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 643 CATGGTCCCGTAGGTTGGGGCCCTGAGGCTGAGAGCTCCGGCTCTGTTGTACACC 702
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 593 AGCCATGTGACCTTTAAACCTATGAAGTATGATGACAGATTCGTGTCAACAGAGAA 652
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 703 TGCAGAGGTTCAGATTCAACATACCCGGGTGTCATGCAACAGCTCCTGCTCAGAGAT 762
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 653 GATGATGTCAAGCAATTCATTGATTAACCTCTACCTCC 691
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DB 763 GCGAGCTGTGAAGAAATTTCTTGAGAAAGCTCGCTCC 801
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RESULT 12
US-09-629-645A-20
; Sequence 20, Application US/09629645A
; Patent No. 6365354

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GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF LYSPHOSPHOLIPASE I EXPRESSION
FILE REFERENCE: RTS-0137
CURRENT APPLICATION NUMBER: US/09/629,645A
CURRENT FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 164
SEQ ID NO 20
LENGTH: 608
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: unsure
LOCATION: 598
OTHER INFORMATION: unknown
NAME/KEY: CDS
LOCATION: (1)...(97)
US-09-629-645A-20

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Query Match      12.8%; Score 90.6; DB 4; Length 608;
Best Local Similarity 91.4%; Pred. No. 3.1e-20;
Matches 96; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 605 CTTTAAACCTATGAAGTATGATGACACAGTTCGTGTCAACAGAGAAATGATGATCA 664
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DB 1 CTTCAAAATCATGAAGGATGATGACAGCTCATGTGTCAGAGAAATGATGATGATCA 60
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QY 665 GCATTTATGATTAATCTTACCTCAATGATGACGTCAC 709
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DB 61 GCATTTATGATTAATGCTCTTACCTCAATGATGATGATGATCA 105
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RESULT 13
US-09-216-001-2
; Sequence 2, Application US/09216001
; Patent No. 6004792
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Puri
APPLICANT: Corley, Neil C.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NEW HUMAN LYSPHOSPHOLIPASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,001
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,862
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0329 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

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; INFORMATION FOR SEQ ID NO: 2:
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308 TGATCAAGAGTGAAGATGGCATTCCTTCTAACAGAAATTATTTGGGA 356

Tue Jan 21 10:18:37 2003

us-09-988-982-2.rni

Page 10

Db 966 TGACGCACTAGAAAAGATCCTATCCCTGAAAACATTACTGTTATAGA 1014

Search completed: January 19, 2003, 03:15:21
Job time : 80 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2003, 01:38:35 ; Search time 100 Seconds
(without alignments)
3161.206 Million cell updates/sec

Title: US-09-988-982-2
Perfect score: 709
Sequence: 1 GCCCGTCGACAGCCCTTGCG.....CCAATTGATTGACGTACATA 709

Scoring table:
Gapop 10.0, Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	707.6	99.8	709	US-09-988-982-2	Sequence 2, Appl1
2	628.4	88.6	2493	US-09-925-299-218	Sequence 218, App
3	589.4	83.1	2417	US-09-813-358-221	Sequence 221, App
4	392.4	55.3	416	US-10-046-935-1369	Sequence 1369, Ap
5	392.4	55.3	416	US-09-878-178-1369	Sequence 1369, Ap
6	230.2	31.1	441	US-09-960-352-3924	Sequence 3924, Ap
7	126	17.8	782	US-09-813-358-220	Sequence 220, App
8	119.8	16.9	461	US-09-813-358-207	Sequence 207, App
9	99.4	14.0	106	US-09-998-598-2083	Sequence 2083, Ap
10	79.2	11.2	105	US-09-796-692-5977	Sequence 5977, Ap
11	55.8	7.9	589	US-09-969-347-51	Sequence 51, Appl
12	55.8	7.9	802	US-09-833-381-1895	Sequence 1895, Ap
13	51.8	7.3	583	US-09-833-381-1894	Sequence 1894, Ap
14	35.6	5.1	396	US-09-853-386-88	Sequence 88, Appl
15	35.6	5.0	6659	US-09-321-987B-1	Sequence 1, Appl1
16	35.2	5.0	561	US-09-833-381-1893	Sequence 1893, Ap
17	35	4.9	116592	US-09-818-512-3	Sequence 3, Appl1
18	34.4	4.9	9824	US-09-853-386-1	Sequence 1, Appl1
19	34.4	4.9	10883	US-09-853-386-13	Sequence 13, Appl1

20 33.8 4.8 1356 10 US-09-967-805-8 Sequence 8, Appl1

21 33.6 4.7 88421 9 US-09-976-059-1 Sequence 1, Appl1

22 32.2 4.5 376 10 US-09-983-965-4282 Sequence 4282, Ap

23 32.2 4.5 29344 10 US-09-464-767-1 Sequence 1, Appl1

24 32.2 4.5 32745 10 US-09-464-767-3 Sequence 3, Appl1

25 32 4.5 945 10 US-09-886-055-360 Sequence 360, App

26 32 4.5 4800 9 US-09-738-626-810 Sequence 810, App

27 31.8 4.5 2000 9 US-09-938-842-3144 Sequence 3144, Ap

28 31.6 4.5 727 10 US-09-910-943-478 Sequence 478, App

29 31.4 4.4 4257 9 US-09-825-2884-1 Sequence 1, Appl1

30 31.2 4.4 289 10 US-09-294-093B-992 Sequence 992, App

31 31.2 4.4 197997 10 US-09-822-246-3 Sequence 3, Appl1

32 31.2 4.4 640681 10 US-09-790-988-1 Sequence 1, Appl1

33 31 4.4 386 10 US-09-783-590-11377 Sequence 11377, A

34 31 4.4 466 10 US-09-864-761-16083 Sequence 16083, A

35 31 4.4 686 9 US-09-930-125-13 Sequence 13, Appl1

36 30.8 4.3 460 10 US-09-791-171-89 Sequence 89, Appl1

37 30.8 4.3 1104 9 US-09-894-844-3 Sequence 91, Appl1

38 30.8 4.3 1200 10 US-09-791-171-91 Sequence 91, Appl1

39 30.8 4.3 1500 10 US-09-922-501-11 Sequence 11, Appl1

40 30.8 4.3 1617 10 US-09-023-588-67 Sequence 67, Appl1

41 30.8 4.3 2606 10 US-09-837-654-7 Sequence 7, Appl1

42 30.8 4.3 2606 10 US-09-837-654-7 Sequence 7, Appl1

43 30.8 4.3 2754 10 US-09-861-801-3 Sequence 3, Appl1

44 30.8 4.3 3439 10 US-09-837-654-6 Sequence 6, Appl1

45 30.8 4.3 3439 10 US-09-837-654-6 Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-988-982-2
; Sequence 2, Appl1 Application US/09988982
; Patent No. US20020081699A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Inventor: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYXOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,982
; FILING DATE: 19-NO. US20020081699A1-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/213,394
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

LIBRARY: KIDN00119
 CLONE: 2676650
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-988-982-2

Query Match 99.8%; Score 707.6; DB 10; Length 709;
 Best Local Similarity 100.0%; Pred. No. 2.9e-211;
 Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCCGTCGACAGCCCTTGGGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCTGTG 60
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DB 1 GCCGTCGACAGCCCTTGGGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCTGTG 60
QY 61 ACCTGAGGCGGTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCATCTGCCCC 120
    |||||||
DB 61 ACCTGAGGCGGTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCATCTGCCCC 120
QY 121 CCGCCCGGAAGGCCACCGCTGGGCTGATTTCTTCATGATGGATGGAGATCTGGGCGCTG 180
    |||||||
DB 121 CCGCCCGGAAGGCCACCGCTGGGCTGATTTCTTCATGATGGATGGAGATCTGGGCGCTG 180
QY 181 TTAGGCTGTGTACATTTAAATATGAACGTGGCTATGCTCTCATGTGTTGATATTATGGGC 240
    |||||||
DB 181 TTAGGCTGTGTACATTTAAATATGAACGTGGCTATGCTCTCATGTGTTGATATTATGGGC 240
QY 241 TTTCACACAGATTCACAGAGATGATCTGGATTTAAACAGCAGCAGCAAAATATTAAG 300
    |||||||
DB 241 TTTCACACAGATTCACAGAGATGATCTGGATTTAAACAGCAGCAGCAAAATATTAAG 300
QY 301 CTTTGATGTATCAGAGAGAGATGAGATGGCATCTCTTAACAGATTAATTTTGGAGGGT 360
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DB 301 CTTTGATGTATCAGAGAGAGATGAGATGGCATCTCTTAACAGATTAATTTTGGAGGGT 360
QY 361 TTTTCTCAGGAGAGCTTTATCTTTATATATCTGCCCTTACACACAGCAGAACTGGCAG 420
    |||||||
DB 361 TTTTCTCAGGAGAGCTTTATCTTTATATATCTGCCCTTACACACAGCAGAACTGGCAG 420
QY 421 GGTGTCACACAGCTTCTTGTCTTCCACTTCGCGGNTCCCTTCCACAGGSKCTATGCG 480
    |||||||
DB 421 GGTGTCACACAGCTTCTTGTCTTCCACTTCGCGGNTCCCTTCCACAGGSKCTATGCG 480
QY 481 GTGTGCTATAGAGATTTCTTATCTTCCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
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DB 481 GTGTGCTATAGAGATTTCTTATCTTCCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
QY 541 CCCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGGATTCACAGCCATG 600
    |||||||
DB 541 CCCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGGATTCACAGCCATG 600
QY 601 TGACCTTTAAACCTATGAAGATGATGACAGATTCGTGCACAGAGAAATGATGATG 660
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DB 601 TGACCTTTAAACCTATGAAGATGATGACAGATTCGTGCACAGAGAAATGATGATG 660
QY 661 TCAAGCAATTCATTTAAACTCTTACCTCCATTCATTTGATGAGCTACTA 709
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DB 661 TCAAGCAATTCATTTAAACTCTTACCTCCATTCATTTGATGAGCTACTA 709

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RESULT 2

US-09-925-299-218
 ; Sequence 218, Application US/09925299
 ; Patent No. US20020055627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA102
 ; CURRENT APPLICATION NUMBER: US/09/925,299
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05883
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; APPLICANT: Stolk, John A.
 ; NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 218
 ; LENGTH: 2493
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-299-218

Query Match 88.6%; Score 628.4; DB 10; Length 2493;
 Best Local Similarity 91.0%; Pred. No. 3.6e-186;
 Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

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QY 1 GCCGTCGACAGCCCTTGGGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCTGTG 60
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DB 26 GCCGTCGACAGCCCTTGGGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCTGTG 85
QY 61 ACCTGAGGCGGTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCATCTGCCCC 120
    |||||||
DB 86 ACCTGAGGCGGTGTATGTGCGGCAATTAACATGTCAACCCCGCTGCCCATCTGCCCC 145
QY 121 CCGCCCGGAAGGCCACCGCTGGGCTGATTTCTTCATGATGGATGGAGATCTGGGCGCTG 175
    |||||||
DB 146 CCGCCCGGAAGGCCACCGCTGGGCTGATTTCTTCATGATGGATGGAGATCTGGGCGCTG 205
QY 176 ----- 175
DB 206 GATGGCGAGAGCCTTTCAGATATCAGAAATTCACATATCAAAATATATCTGCCCATG 265
QY 176 -GCCTGTAGCCCTGTACATTAATATGAACGTGGCTATGCCCTCATGGTTGATATTA 234
    |||||||
DB 266 CGCCTGTAGCCCTGTACATTAATATGAACGTGGCTATGCCCTCATGGTTGATATTA 325
QY 235 TTGGGCTTTCACAGATTCACAGAGAGATGATCTGGGATTTAAACAGCAGCAGAAAAATA 294
    |||||||
DB 326 TTGGGCTTTCACAGATTCACAGAGAGATGATCTGGGATTTAAACAGCAGCAGAAAAATA 385
QY 295 TAAAGCTTTGATGATCAGAAATGAAGATGATCTCTTCAACAGAAATATTTTGG 354
    |||||||
DB 386 TAAAGCTTTGATGATCAGAAATGAAGATGATCTCTTCAACAGAAATATTTTGG 445
QY 355 GAGGCTTTCACAGAGAGAGCCTTATCTTATATCTGCTTACACACAGCAGAAAC 414
    |||||||
DB 446 GAGGCTTTCACAGAGAGAGCCTTATCTTATATCTGCTTACACACAGCAGAAAC 505
QY 415 TGGCAGGTGTCAGTCACTGATCTTCTTCCACTTCGCGGNTCCCTTCCACAGGK 474
    |||||||
DB 506 TGGCAGGTGTCAGTCACTGATCTTCTTCCACTTCGCGGNTCCCTTCCACAGGK 565
QY 475 CTATCGGTGGTCTAATAGATATTTCTATTCACAGTGCACAGGGGATTTGACCCCT 534
    |||||||
DB 566 CTATCGGTGGTCTAATAGATATTTCTATTCACAGTGCACAGGGGATTTGACCCCT 625
QY 535 TGGTCCCTGATGTTGGTCTCTTACGGTGAAGAAAACTAAACATTTGGTGAATCCAG 594
    |||||||
DB 626 TGGTCCCTGATGTTGGTCTCTTACGGTGAAGAAAACTAAACATTTGGTGAATCCAG 685
QY 595 CCAATGTACCTTTAAACCTATGAAGTATGATGACAGAGTTCGTGCACAGAGAAATGA 654
    |||||||
DB 686 CCAATGTACCTTTAAACCTATGAAGTATGATGACAGAGTTCGTGCACAGAGAAATGA 745
QY 655 TGGATGTACAGCAATTCATTTAAACTCTACCTCCCAATGATTTGAGCTACTA 709
    |||||||
DB 746 TGGATGTACAGCAATTCATTTAAACTCTACCTCCCAATGATTTGAGCTACTA 800

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RESULT 3

US-09-813-358-221
 ; Sequence 221, Application US/09813358
 ; Patent No. US20020048759A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Stolk, John A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

```

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
; FILE REFERENCE: 210121.501
; CURRENT APPLICATION NUMBER: US/09/813,358
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-358-221

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Query Match      83.1%; Score 589.4; DB 10; Length 2417;
Best Local Similarity 90.5%; Pred. No. 5,5e-174;
Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

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OY 100 GCGTCCCGCCGATGCTGCGCGCGCGCGGAGGCGCACCGCGGGTGATTTTCTCGATG 159
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DB 61 GCGTCCCGCCGATGCTGCGCGCGCGCGGAGGCGCACCGCGGGTGATTTTCTCGATG 120
OY 160 GATTGGAGATACCTG-----175
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DB 121 GATTGGAGATACCTGCGGAGGATGGGAGAGCGTTTGCAGATGACGAAGTTACATA 180
    |||||||
OY 176 -----GCCTGTAGGCTGTTACCTTAATATGACGTGCTA 213
    |||||||
DB 181 TCAATATATCTGCCCGCATGCGCTGTAGGCTGTACATTAATATGACGTGCTA 240
OY 214 TGCCTCATGTTGATATATTTGGGCTTTCACAGATTCACAGAGGATGAATCTGGGA 273
    |||||||
DB 241 TGCTTCATGTTGATATATTTGGGCTTTCACAGATTCACAGAGGATGAATCTGGGA 300
OY 274 TTAACAGGACAGCAAAATATAAAGCTTGATGATCAAGAAGTGAAGATGGCATTC 333
    |||||||
DB 301 TTAACAGGACAGCAAAATATAAAGCTTGATGATCAAGAAGTGAAGATGGCATTC 360
OY 334 CTTCTACAGAAATATTTTGGGAGGTTTCTCAGGAGGAGCTTTATCTTATATACGTG 393
    |||||||
DB 361 CTTCTACAGAAATATTTTGGGAGGTTTCTCAGGAGGAGCTTTATCTTATATACGTG 420
OY 394 CCTTACACAGCAAGAACTGCGAGGTGCTACAGCACTGATGTTCTGTTCCACTTC 453
    |||||||
DB 421 CCTTACACAGCAAGAACTGCGAGGTGCTACAGCACTGATGTTCTGTTCCACTTC 480
OY 454 GGGNTCTCTTCCACAGGAGKCTATCGTGTGCTAATAGATATTTCTATCTCCAGT 513
    |||||||
DB 481 GGGCTCTCTTCCACAGGAGGTCTATCGTGTGCTAATAGATATTTCTATCTCCAGT 540
OY 514 GCCACGGGATTTGACCCCTTGTGCTCCCTGATGTTTGTCTTACGGTGAAGAAC 573
    |||||||
DB 541 GCCACGGGATTTGACCCCTTGTGCTCCCTGATGTTTGTCTTACGGTGAAGAAC 600
OY 574 TAAAAACATTTGTAATCCAGCAAGTGAACCTTAAAAACCTATAGAGGATGATGACA 633
    |||||||
DB 601 TAAAAACATTTGTAATCCAGCAAGTGAACCTTAAAAACCTATAGAGGATGATGACA 660
OY 634 GTTCGTGCAACAGAAATGATGATGCAAGCAATTCATGATTAACCTCTACTCCAA 693
    |||||||
DB 661 GTTCGTGCAACAGAAATGATGATGCAAGCAATTCATGATTAACCTCTACTCCAA 720
OY 694 TTGATGACGTCACTA 709
    |||||||
DB 721 TTGATGACGTCACTA 736

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RESULT 4
US-10-046-935-1369/c
; Sequence 1369, Application US/10046935
; Patent No. US20020156011A1

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; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secretist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1369
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-1369

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Query Match      55.3%; Score 392.4; DB 9; Length 416;
Best Local Similarity 99.0%; Pred. No. 7.4e-113;
Matches 393; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 313 AGAAGTGAAGATGCGCATTCCTTCAAGAAATATTTGGGAGGTTTCTCAGGAG 372
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DB 416 AGAAGTGAAGATGCGCATTCCTTCAAGAAATATTTGGGAGGTTTCTCAGGAG 357
OY 373 GACCTTATCTTATATATCTGCGCTTACACAGACAGCAAACTGGAGGTGCAC 432
    |||||||
DB 356 GACCTTATCTTATATATATCTGCGCTTACACAGACAGCAAACTGGAGGTGCAC 297
OY 433 TCAGTTCTCTGCTTCCACTTCCGGGNTTCTTCCACAGGKCTATCGGTGCTAATA 492
    |||||||
DB 296 TCAGTTCTGCTTCCACTTCCGGGNTTCTTCCACAGGKCTATCGGTGCTAATA 237
OY 493 GAGATATTTCTATCTTCCACTTCCGGGNTTCTTCCACAGGKCTATCGGTGCTAATA 552
    |||||||
DB 236 GAGATATTTCTATCTTCCACTTCCGGGNTTCTTCCACAGGKCTATCGGTGCTAATA 177
OY 553 GTTCTCTTACGTTGGAAGAACTAAAACTATGTTGATTCAGCAATGACCTTTAAA 612
    |||||||
DB 176 GTTCTCTTACGTTGGAAGAACTAAAACTATGTTGATTCAGCAATGACCTTTAAA 117
OY 613 CCTATGAGGTATGATGACAGTTCGTGTCACAGAAATGATGATCAACCAATTC 672
    |||||||
DB 116 CCTATGAGGTATGATGACAGTTCGTGTCACAGAAATGATGATGATGATCAACCAATTC 57
OY 673 TTGATAAATCTCTACCTCCCAATGATGAGTCACTA 709
    |||||||
DB 56 TTGATAAATCTCTACCTCCCAATGATGAGTCACTA 20

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RESULT 5
US-09-878-178-1369/c
; Sequence 1369, Application US/09878178
; Patent No. US2002017752A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1369
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-1369

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Query Match 55.3%; Score 392.4; DB 9; Length 416;
 Best Local Similarity 99.0%; Pred. No. 7.4e-113;
 Matches 393; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 313 AAGAAGGAAGATGCGATTCCTTCTTACAGAAATTTTGGAGGGTTTTCAGGGAG 372
 DB 416 AAGAAGGAAGATGCGATTCCTTCTTACAGAAATTTTGGAGGGTTTTCAGGGAG 357
 QY 373 GAGCTTATCTTATATACAGCCCTTACACAGAGAAATGAGAGGTGCTACGAC 432
 DB 356 GAGCTTATCTTATATACAGCCCTTACACAGAGAAATGAGAGGTGCTACGAC 297
 QY 433 TCAGTTTCTTCTCCACTTCGCGGNTTCTTTCACAGGGGCTATCGGTGCTAATA 492
 DB 296 TCAGTTTCTTCTCCACTTCGCGGNTTCTTTCACAGGGGCTATCGGTGCTAATA 237
 QY 493 GAGATATCTTCTTCTCCACTTCGCGGNTTCTTTCACAGGGGCTATCGGTGCTTGG 552
 DB 236 GAGATATCTTCTTCTCCACTTCGCGGNTTCTTTCACAGGGGCTATCGGTGCTTGG 177
 QY 553 GTTCTCTTACGGTGAAGAAATCTAAAAACATTTGGTGAATCCAGCCATGTGACCTTAAAA 612
 DB 176 GTTCTCTTACGGTGAAGAAATCTAAAAACATTTGGTGAATCCAGCCATGTGACCTTAAAA 117
 QY 613 CCTATGAAGGTATGATGACAGATGCTGTCACAGAGAAATGATGATCAACCAATTCA 672
 DB 116 CCTATGAAGGTATGATGACAGATGCTGTCACAGAGAAATGATGATCAACCAATTCA 57
 QY 673 TTGATTAACCTCTACCTCCCAATGATGTAGCTACCTA 709
 DB 56 TTGATTAACCTCTACCTCCCAATGATGTAGCTACCTA 20

RESULT 6

US-09-960-352-3924
 ; Sequence 3924, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Tao, Nengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathialagan, Nagappan
 ; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
 ; FILE REFERENCE: 16511.006/37-21(10298)C
 ; CURRENT APPLICATION NUMBER: US/09/960,352
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 15112
 ; SEQ ID NO 3924
 ; LENGTH: 441
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 17-LIB34-018-Q1-E1-E1
 US-09-960-352-3924

Query Match 31.1%; Score 220.2; DB 10; Length 441;
 Best Local Similarity 76.1%; Pred. No. 5.3e-59;
 Matches 316; Conservative 0; Mismatches 33; Indels 66; Gaps 1;

QY 69 CGGTGATGTGGCGCAATTAACATGCAACCCCGCTGCGCGCATGCTGCCCGCGCGG 128
 DB 25 CGGTGATGTGGCGCAATTAACATGCTGCGCGCATGCTGCCCGCGCGGCT 84
 QY 129 AAGGCCACGCTGCGGATTTTCGTCATGATGAGATGGAGATCTGGGGCT----- 179
 DB 85 AAGGCCACGCTGCGGATTTTCGTCATGATGAGATGGAGATGAGATGAGGCA 144
 QY 180 -----GTT 182
 DB 145 GAGCCTTTGCGGAAATCAAGAGCCGCAATCAATACATCTGCCGCGCGGCTT 204
 QY 183 AGCCCTGTTACATTAATATGAAGCTGGCTATGCCCTTCAATGTTGATATATATGGGCTT 242

DB 205 ATGCCGTGAACATTAATAATGAACATGGCCATGCCATCATGGTTTGACATTATGGGCTT 264
 QY 243 TCACAGATTCACAGAGATGAATCTGGATTAACAGAGCAGAAATATAAAGCT 302
 DB 265 TCACAGATTCACAGAGATGAATCTGGATTAACAGAGCAGAAATATAAAGCT 324
 QY 303 TTGATGATCAAGAGATGAAGATGGCATTCCTTCTTAACAGAAATATTTTGGAGGGTTT 362
 DB 325 TTGATGATCAAGAGATGAAGATGGCATTCCTTCTTAACAGAAATATTTTGGAGGGATTT 384
 QY 363 TCTCAGGAGAGGCTTTATCTTATATACAGGCTCTTACACAGAGCAAGAACTGG 417
 DB 385 TCTCAGGAGAGGCTTTATCTTGTACAGGCTCTGACCAACACAGAGAACTGG 439

RESULT 7

US-09-813-358-220
 ; Sequence 220, Application US/09813358
 ; Patent No. US20020048759A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Stolk, John A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.501
 ; CURRENT APPLICATION NUMBER: US/09/813,358
 ; CURRENT FILING DATE: 2001-03-21
 ; NUMBER OF SEQ ID NOS: 222
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 220
 ; LENGTH: 782
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-358-220

Query Match 17.8%; Score 126; DB 10; Length 782;
 Best Local Similarity 100.0%; Pred. No. 2.2e-29;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 GGTGATCCAGCCATGACCTTAAACATGAAGGTATGATGACAGTTCGTGCA 643
 DB 1 GGTGATCCAGCCATGACCTTAAACATGAAGGTATGATGACAGTTCGTGCA 60
 QY 644 ACAGAAATGATGATGTCACAGCAATTCATGATTAACCTCTACCTCAATGATGACG 703
 DB 61 ACAGAAATGATGATGTCACAGCAATTCATGATTAACCTCTACCTCAATGATGACG 120
 QY 704 TCACCTA 709
 DB 121 TCACCTA 126

RESULT 8

US-09-813-358-207
 ; Sequence 207, Application US/09813358
 ; Patent No. US20020048759A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Stolk, John A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.501
 ; CURRENT APPLICATION NUMBER: US/09/813,358
 ; CURRENT FILING DATE: 2001-03-21
 ; NUMBER OF SEQ ID NOS: 222
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 207
 ; LENGTH: 461
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-358-207


```

RESULT 13
US-09-833-381-1894
; Sequence 1894, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs

```

RESULT 15
US-09-321-987B-1


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; Sequence 1, Application US/09321987B
; Patent No. us20020102210A1
; GENERAL INFORMATION:
; APPLICANT: Kimble, Judith E
; APPLICANT: Bluelloch, Robert H
; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
; FILE REFERENCE: 960296,95386
; CURRENT APPLICATION NUMBER: US/09/321,987B
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,170
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/129,023
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6659
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6450)
; US-09-321-987B-1
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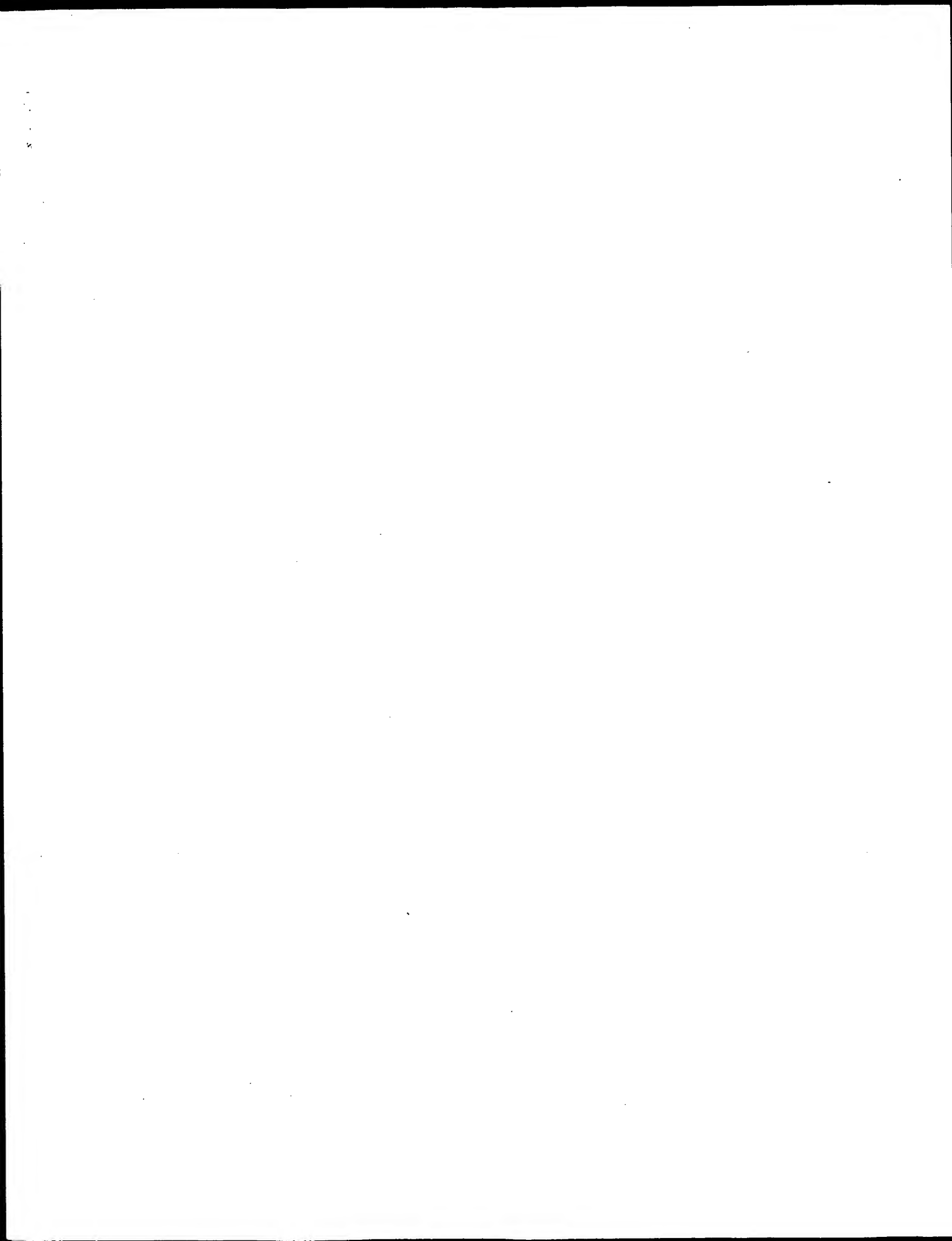
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Query Match          5.0%; Score 35.6; DB 10; Length 6659;
Best Local Similarity 54.6%; Pred.No.1.5;
Matches 71; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 222 TGGTTGATATTATTTGGGCTTTCACACAGATTTCACAGAGATGAATCTGGGATTAAACAG 281
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 5752 TGTTTGAAGAAGAAATTCCTCCGTCACACTGTGACGAGAGCTTAATCTCAGATGTTAG 5811

QY 282 GCAGCAGAAATATATAAGCTTGTGATGATCAAGAGTGAAGATGGCATTCCTTCTAAC 341
    || ||| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 5812 GCTAAAGATGCAATTTACACTATCTCTGTGACGAGATTCACCTAATGAATTTATGTCAT 5871

QY 342 AGAATTATTT 351
    ||| | | |
DB 5872 CGAATGAATT 5881
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Search completed: January 19, 2003, 03:17:15
Job time : 111 secs



[illegible]

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3	577.4	81.4	774	9	AU133073	AU133073	
4	569	80.3	765	12	B6722409	6026593642	
5	563	79.4	740	12	B6773497	602720223	
6	563	79.4	1061	13	B6475259	A69NCOURR	

	RESULT 1			
LOCUS	AU132495			
DEFINITION	AU132495 NT2RP3 Homo sapiens CDNA clone NT2RP3004603 5', mRNA sequence.	796 bp	mRNA	linear EST 01-AUG-2000
ACCESSION	AU132495			
VERSION	AU132495.1	GI:10992849		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 796)			
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Negai,T., Sugano,S. and Isogai,T.			
TITLE	HRI human CDNA project			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.			

FEATURES
source

Location/Qualifiers
1. .796
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2R3004603"
/clone_11b="NT2R3"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3: mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 191 a 188 c 196 g 214 t 7 others
ORIGIN

Query Match 82.3%; Score 583.6; DB 9; Length 796;
Best Local Similarity 89.5%; Pred. No. 4.5e-163;
Matches 696; Conservative 1; Mismatches 11; Indels 70; Gaps 4;

1 GCCGCTGCAGCCGCTTGGGCGCGCGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
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5 GCCGCTGCAGCCGCTTGGGCGCGCGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 64
|||||
61 AGCTGAGGGGTATGTGCGGCAATACATGTCACACCCGCTGCGCGCATCGCCCG 120
|||||
65 AGCTGAGGGGTATGTGCGGCAATACATGTCACACCCGCTGCGCGCATCGCCCG 124
|||||
121 CGCCCGGAGGAGCCAGCGCTGCGGTGATTTCTGATGATTTGGAGATACGTTG 175
|||||
125 CGCCCGGAGGAGCCAGCGCTGCGGTGATTTCTGATGATTTGGAGATACGTTG 184
|||||
176 ----- 175

185 GATGGGAGAGAGCTTTGCGAGGTATCAGAAATTCATATCAATATATGCGCGCATG 244
176 -GCCGTGAGGCTGTACATTAATATGAGCGTATGCGCTTCAATGTTGATATTA 234
|||||
245 CGCCTTTAGGCTGTATTAATTAATTAACGTGCGCTTCAATGTTGATATTA 304
|||||
235 TTGGGCTTTACACAGATTCACAGAGAGATGAATCTGGGATTAACAGCAGCAAAATA 294
|||||
305 TTGGGCTTTACACAGATTCACAGAGAGATGAATCTGGGATTAACAGCAGCAAAATA 364
|||||
295 TAAACCTTGTATGATCAAGAGATGAAGATGGCATTCCTTCAACAAATATTTTGG 354
|||||
365 TAAACCTTGTATGATCAAGAGATGAAGATGGCATTCCTTCAACAAATATTTTGG 424
|||||
355 GAGGCTTTCTCAGGAGAGAGCTTTATCTTATATCTCCCTTACACAGCAGCAAAAC 414
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425 GAGGCTTTCTCAGGAGAGAGCTTTATCTTATATCTCCCTTACACAGCAGCAAAAC 484
|||||
415 TGGCAGGTGTACGTCACTGATTTCTTCTTCCTTCACCTTGGGNTTCTTCCACAGGKC 474
|||||
485 TGGCAGGTGTACGTCACTGATTTCTTCTTCCTTCACCTTGGGNTTCTTCCACAGGKC 544
|||||
475 CTATCGGTGTGTATATAGATATTTCTATCTCCAGTCCAGCAGGAGGATTTGACCTT 534
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545 CTATCGGTGTGTATATAGATATTTCTATCTCCAGTCCAGCAGGAGGATTTGACCTT 604
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535 TGGTCCCGCTGATTTGGTCTCTTACCGTGGAAAAATTAACATTTGGTGAATCCAG 594
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605 TGGTCCCGCTGATTTGGTCTCTTACCGTGGAAAAATTAACATTTGGTGAATCCAG 664
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595 CCAATGTGACCTTTAAAAACCTATGAAGATGATGCAC -AGTTCGTGCAC -AGGAAT 652
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665 CCAATGTGACCTTTAAAAACCTATGAAGATGATGCAC -AGTTCGTGCAC -AGGAAT 724
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653 GATGATGTCAACATTCATGATTAATCTTAC -TCCATTTGATGAGTCTCT 708
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725 GATGATGTCAACATTCATGATTAATCTTAC -TCCATTTGATGAGTCTCT 782
|||||

RESULT 2
BG696407 919 bp mRNA linear EST 07-MAY-2001
LOCUS BG696407

DEFINITION 602659503F1 NCL_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:480265 5',
mRNA sequence.
ACCESSION BG696407
VERSION BG696407.1 GI:13961520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 919)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LRAM10697 row: e column: 02
High quality sequence stop: 807.

FEATURES
source

1. .919
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:480265"
/clone_11b="NCL CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Skin; Vector: PCMV-SpOrf6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCL_CGAP Library."

BASE COUNT 241 a 202 c 212 g 264 t
ORIGIN

Query Match 81.9%; Score 580.4; DB 12; Length 919;
Best Local Similarity 90.4%; Pred. No. 4.3e-162;
Matches 657; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

49 GCTTGGCGGTGAGCTGAGCGGTGTATGTGCGCAATTAACATGTCACACCCGCTGCCG 108
|||||
1 GCTTGGCGGTGAGCTGAGCGGTGTATGTGCGCAATTAACATGTCACACCCGCTGCCG 60
|||||
109 CCATGTCGCCCGCGCGCGGAGGCCACCGCTGCGTGAATTTCTTCATGATTTGGAG 168
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61 CCATGTCGCCCGCGCGGAGGCCACCGCTGCGTGAATTTCTTCATGATTTGGAG 120
|||||
169 ATACTGG----- 175
|||||
121 ATACTGGGCGACGATGGGAGAGAGCTTTGCGAGGTATCAGAAATTCATTAATATA 180
|||||
176 -----GCCGTGAGGCTGTACATTAATATGAGCGTATGCGCTTCAAT 222
|||||
181 TCTGCGCGCATGCGCTTATGCGCTGTACATTAATATGAGCGTATGCGCTTCAAT 240
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223 GGTTCATATTTATTTGGGCTTTCACAGATTCACAGAGATGAATCTGGGATTAACAGG 282
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241 GGTTCATATTTATTTGGGCTTTCACAGATTCACAGAGATGAATCTGGGATTAACAGG 300
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283 CAGCAGAAATATTAAGCTTTGATTTGATCAAGAGTGAAGAAATGGCATTCCTCTAACA 342
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301 CAGCAGAAATATTAAGCTTTGATTTGATCAAGAGTGAAGAAATGGCATTCCTCTAACA 360
|||||
343 GAATATTTTGGGAGGTTTCTCAGGAGAGGCTTATCTTATATATCTCCCTTACCA 402
|||||
361 GAATATTTTGGGAGGTTTCTCAGGAGAGGCTTATCTTATATATCTCCCTTACCA 420
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403 CACAGCAAAACTGCGAGGTGTCACGTCACTGATTTCTTCTTCCTTCACTTGGGNTTCT 462
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421 CACAGCAAAACTGCGAGGTGTCACGTCACTGATTTCTTCTTCCTTCACTTGGGNTTCT 480
|||||

OY	463	TTCCACAGGKCCCTTTCGCTGCTATPAGATATTTCTATTCACAGTCCACGGGG	522
Db	461	TTCCACAGGGTCCTATCGGTGTGCTAATAGAGATATTTCTATTCAGTCCACGGGG	540
OY	523	ATTGTGACCCCTTTGGTTCCTCGATGTTTGTCTCTTAACGGTGGAAAAACCTAAAAACAT	582
Db	541	ATTGTGACCCCTTTGGTTCCTCGATGTTTGTCTCTTAACGGTGGAAAAACCTAAAAACAT	600
OY	583	TGGTGAATCCAGCCCAATGTGACCTTTAAACCTATGAAGGTATGATGCACTTCGTGTGC	642
Db	601	TGGTGAATCCAGCCCAATGTGACCTTTAAACCTATGAAGGTATGATGCACTTCGTGTGC	660
OY	643	AACAGGAATGATGTGATGTCAAGCAATTCATTTGATGATAACTCCTACCTCCAAATTTGATTGAC	702
Db	661	AACAGGAATGATGTGATGTCAAGCAATTCATTTGATGATAACTCCTACCTCCAAATTTGATTGAC	720
OY	703	GTCACTA 709	
Db	721	GTCACTA 727	

RESULT 3	774 bp	mRNA	linear	EST 01-AUG-2002
AUI33073				
LOCUS				
DEFINITION	AUI33073	NT2RP4	Homo sapiens cDNA clone NT2RP4001208 5',	mRNA
ACCESSION	sequence.			
VERSION	AUI33073			
KEYWORDS	AUI33073.1	GI:10993612		
SOURCE	EST.			
	human.			

REFERENCE
AUTHORS
Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 774)

TITLE

JOURNAL
COMMENT
Unpublished (2000)
Contact: Takao Isogai

Salvo, A., Iadamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuno, Y., Isogai, T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end ones pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Virus Research Institute.

FEATURES	Location/Qualifiers
source	1. .774

BASE COUNT	ORIGIN
197 a	173 c 185 g 216 t 3 others

Query Match	81.4%;	Score 577.4;	DB 9;	Length 774;
Best Local Similarity	90.2%;	Pred. No. 3.2e-161;		
Matches 665; Conservative	1;	Mismatches 4;	Indels 67;	Gaps 2

QY 40 CTTCCTTCCGCTTGCGGTGAGACTGAGCGGGTGTATGTGCGGCATTAACATGTCAACC 99
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Dd 1 CTTCCTTCCGCTTGCGGTGAGACTGAGCGGGTGTATGTGCGGCATTAACATGTCAACC 60

QY	100	CGCTCCCGCCACATGCTGGCCCGCCCGCCGGAAGGCCACCCCTGCGGGATTTTCCCTGCATG	159
Db	61	CGCTCCCGCCACATGCTGGCCCGCCCGCCGGAAGGCCACCCCTGCGGGATTTTCCCTGCATG	120
QY	160	GATTGGAGATATCTGTG-----	175
Db	121	GATTGGAGATATCTGTGGCGACGATGGGCGAAGAACCTTTCCAGGTATCAGAACGTTCCACATA	180
QY	176	-----GCTGTTAGCCCTGTTCATTAAATATGAACGTGGCTTA	213
Db	181	TCAATATATCTGCCCGCATGGCCCGCTTAGGCCCTGTTCATTAAATATGAACGTGGCTTA	240
QY	214	TGCTTCATGCTTTATATATTTGGGCTTTCACCAAGATTCACAGAGAGATGTAATCTGGGA	273
Db	241	TGCTTCATGCTTTATATATTTGGGCTTTCACCAAGATTCACAGAGAGATGTAATCTGGGA	300
QY	274	TTAAACAGGCGACGAAAAATATAAAGCTTGATATGATCAACAGAGAGAAATGGCATTC	333
Db	301	TTAAACAGGCGACGAAAAATATAAAGCTTGATATGATCAACAGAGAGAAATGGCATTC	360
QY	334	CTTCTAACAGATTTATTTTGGGAGGCTTTTCACAGGAGAGACCTTATATTATATACG	393
Db	361	CTTCTAACAGATTTATTTTGGGAGGCTTTTCACAGGAGAGACCTTATATTATATACG	420
QY	394	CCCTTACACACAGCAGAAACTGGCAGGTGTCACATGCATCGATTTCTTGCCTCCACTTC	453
Db	421	CCCTTACACACAGCAGAAACTGGCAGGTGTCACATGCATCGATTTCTTGCCTCCACTTC	480
QY	454	GCGATTCTTTCCACAGGAGKCTATGCGTGTGCTTAATAGATATTTCTATTTCCAGT	513
Db	481	GCGATTCTTTCCACAGGAGKCTATGCGTGTGCTTAATAGATATTTCTATTTCCAGT	540
QY	514	GCCACGGGAGTTGTACCCCTTTGGTCCCGCTATGTTGGTCTCTGTACGGTGAAGAAAC	573
Db	541	GCCACGGGAGTTGTACCCCTTTGGTCCCGCTATGTTGGTCTCTGTACGGTGAAGAAAC	600
QY	574	TAAAAACATTTGGTGAATCCAGCCAAATGTACCTTTAAAAACCTATGAAGTATGATGAC-	632
Db	601	TAAAAACATTTGGTGAATCCAGCCAAATGTACCTTTAAAAACCTATGAAGTATGATGAC	660
QY	633	AGTTGCTGTCAACAGGAAATGATGGATGTCAAGCAATTCATTTGATTAACCTCTACCTCCA	692
Db	661	AGTTGCTGTCAACAGGAAATGATGGATGTCAAGCAATTCATTTGATTAACCTCTACCTCCA	720
QY	693	ATTGATTGACGTCACTA 709	
Db	721	ATTGATTGACGTCACTA 737	

LOCUS	BG722409	765 bp	mRNA	linear	EST 08-MAY-2001
DEFINITION	60269364221	NIH_MGC_97	Homo sapiens cDNA clone IMAGE:4825691	5',	

mRNA sequence.
 ACCESSION BG722409
 VERSION BG722409.1 GI:14001608
 KEYWORDS EST.

SOURCE ORGANISM	human.	Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Felis catus

REFERENCE	1 (bases 1 to 765)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/Trb4.htm

COMMENT	CONTACT: Robert Straub
JOURNAL	Unpublished (1999)
TITLE	National Institutes of

CONTACT: ROBERT STRAUSS
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mike

Issue Encouragement, FNA
CDNA Library Preparati
Toshiyuki and Piero Carr

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LRAM10739 row: d column: 12

High quality sequence stop: 712.

Location/Qualifiers

1..765

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4825691"

/clone_id="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3', size-selected for average insert size 2.2 kb and normalized to ROP 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 179 a 187 c 195 g 204 t

ORIGIN

Query Match 80.3%; Score 569; DB 12; Length 765;
Best Local Similarity 89.3%; Pred. No. 1e-158;
Matches 673; Conservative 1; Mismatches 12; Indels 68; Gaps 3;

OY 1 GCCGTCGACGCGCTTGGGCGGCGGCGCGCGCTTCTTCCCTTGGCGCTGTG 60
|||||
DB 10 GCCGTCGACGCGCTTGGGCGGCGGCGGCGCGCTTCTTCCCTTGGCGCTGTG 69
OY 61 AGCTGAGGCGGTATGTCGCGCATATACATGCAACCCGCGCGCATCGGCCG 120
|||||
DB 70 AGCTGAGGCGGTATGTCGCGCATATACATGCAACCCGCGCGCATCGGCCG 129
OY 121 CGCGCGGAAAGCCACCGCTGCGGTGATTTTCCCTCATGATGGAGATCTGG----- 175
|||||
DB 130 CGCGCGGAAAGCCACCGCTGCGGTGATTTTCCCTCATGATGGAGATCTGGCGACG 189
OY 176 ----- 175
DB 190 GATGGGACAGACCTTGGAGGTATCAGAGTTCAATATCAATATATCTGCCGATG 249
OY 176 -GCCGTGAGCGCTTACATTAATATGAAGTGGCTATGCTTCAATGTTGATATTA 234
|||||
DB 250 CGCGTGTAGCGCTTACATTAATATGAAGTGGCTATGCTTCAATGTTGATATTA 309
OY 235 TTGGGCTTACACGATTCACAGAGAGATGAAATGCGATTAAACAGGACAGAAATA 294
|||||
DB 310 TTGGGCTTACACGATTCACAGAGAGATGAAATGCGATTAAACAGGACAGAAATA 369
OY 295 TAAACCTTGAATGATCAGAGATGAAGATGGCATCTCTTAACAGATTAATTTTGG 354
|||||
DB 370 TAAACCTTGAATGATCAGAGATGAAGATGGCATCTCTTAACAGATTAATTTTGG 429
OY 355 GAGGTTTTCTCAGGAGAGAGCTTTATCTTATATACCTCCCTTACACAGCAAGAAAC 414
|||||
DB 430 GAGGTTTTCTCAGGAGAGAGCTTTATCTTATATACCTCCCTTACACAGCAAGAAAC 489
OY 415 TGGCAGGTGTCACGACATGATTTTCTTCCATCTTGGGAGTCTTTTCCACAGGCGC 474
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DB 490 TGGCAGGTGTCACGACATGATTTTCTTCCATCTTGGGAGTCTTTTCCACAGGCGC 549
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DB 550 CTATCGGTGTCATTAAGATATTTCTATCTCCAGGCGACAGGAGATGGAGCCCTT 609
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DB 610 TGGTTCCTCCGATGTTGTTCTTACGCTGGAAGAAATTAAGATGATGATCCAG 668
OY 595 CCAATGTGACCTTTAAACCTATGAAGGTATGATGACAGGTTCTGTCAACAGGAATGA 654

DB 669 CCAATGTGACCTTTAAACCTATGAAGGTATGATGACAGGCTGTGTACAGGAATGA 728
OY 655 TGGG-TGTCAGACATTCATGATTAACCTTCAC 687
DB 729 TGGAGTGTCAAGCAATTCCTGATTAACCTTTAC 762

RESULT 5

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

TISSUE

CDNA

CDNA

CDNA

CDNA

CDNA

CDNA

CDNA

CDNA

CDNA

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CDNA

CDNA

CDNA

CDNA

CDNA

CDNA

740 bp mRNA linear EST 15-MAY-2001

602720223F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4837420 5',

mRNA sequence.

NIH-MGC http://imgc.ncl.nih.gov/.

1 (bases 1 to 740)

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@pds-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihai

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LRAM10769 row: m column: 05

High quality sequence stop: 725.

Location/Qualifiers

1..740

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/db_xref="taxon:9606"

/clone="IMAGE:4837420"

/clone_id="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescript (modified

pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcgag

size-selected for average insert size 2.2 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 168 a 179 c 197 g 196 t

ORIGIN

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Best Local Similarity 89.7%; Pred. No. 6.2e-157;
Matches 642; Conservative 1; Mismatches 7; Indels 66; Gaps 1;

OY 1 GCCGTCGACGCGCTTGGGCGGCGGCGCGCGCTTCTTCCCTTGGCGCTGTG 60
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DB 23 GCCGTCGACGCGCTTGGGCGGCGGCGGCGCGCTTCTTCCCTTGGCGCTGTG 82
OY 61 AGCTGAGGCGGTATGTCGCGCATATACATGCAACCCGCGCGCATCGGCCG 120
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DB 83 AGCTGAGGCGGTATGTCGCGCATATACATGCAACCCGCGCGCATCGGCCG 142
OY 121 CGCGCGGAAAGCCACCGCTGCGGTGATTTTCCCTCATGATGGAGATCTGG----- 175
|||||
DB 143 CGCGCGGAAAGCCACCGCTGCGGTGATTTTCCCTCATGATGGAGATCTGGCGACG 202
OY 176 ----- 175

Db 203 GATGGCAGAGACCTTTGAGGTATCAGAAAGTTCAATATATATCTGCCGCGATG 262
 QY 176 -GCTGTAGGCGCTTACATTAATATGAAGCTATGCTATGCTCATGTTTGTATTA 234
 Db 263 CGCCTGTAGGCGCTTACATTAATATGAAGCTATGCTATGCTCATGTTTGTATTA 322
 QY 235 TTGGGCTTTACACAGATTACAGAGAGATGAATCTGGATTAAACAGCAGCAGAAATA 294
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 QY 295 TAAAGCTTTGATATCAAGAAGTGAAGATGATCTTCTTACAGAAATTTATTTGG 354
 Db 383 TAAAGCTTTGATATCAAGAAGTGAAGATGATCTTCTTACAGAAATTTATTTGG 442
 QY 355 GAGGCTTTCTCAGGAGAGCTTTATCTTATATACAGCCCTTACACAGCAGAAAC 414
 Db 443 GAGGCTTTCTCAGGAGAGCTTTATCTTATATACAGCCCTTACACAGCAGAAAC 502
 QY 415 TGGCAGGTGTCACTGACCTAGTTTCTGCTCCACTTCCGAGTTTCTTTCCACAGGAGC 474
 Db 503 TGGCAGGTGTCACTGACCTAGTTTCTGCTCCACTTCCGAGTTTCTTTCCACAGGAGC 562
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 Db 623 TGGTCCCTGATGTTTGGTCTCTTACGGTGAAGAAACATAAATGTTGATCCAG 682
 QY 595 CCAATGTACCTTTAAACCTATGAAGATGATGACAGCTGCTGTCAACAGGAA 650
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RESULT 6
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 ACCESSION BM475259
 VERSION BM475259.1 GI:18524301
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1061)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: gsrabs-r@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLAM2334 row: b column: 17
 High quality sequence stop: 618.

FEATURES

Location/Qualifiers
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 /clone="IMAGE:5578672"
 /clone_lib="NIH_MGC_67"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Library constructed by Life

Technologies."
 BASE COUNT 281 a 228 c 229 g 319 t 4 others
 ORIGIN

Query Match 79.4%; Score 563; DB 13; Length 1061;
 Best Local Similarity 89.5%; Pred. No. 7.1e-157;
 Matches 642; Conservative 1; Mismatches 8; Indels 66; Gaps 1;

QY 59 TGACCTGAGCGGTGTATGTGGCGCAATATACATGTCACCCCGCTGCCCATCTGCC 118
 Db 1 TGACCTGAGCGGTGTATGTGGCGCAATATACATGTCACCCCGCTGCCCATCTGCC 60
 QY 119 CGCGCGCCGGAAGGCCACCCGCTGGGTGATTTTCTCATGATGATGGAGATCTGG- 175
 Db 61 CGCGCGCCGGAAGGCCACCCGCTGGGTGATTTTCTCATGATGATGGAGATCTGG 120
 QY 176 ----- 175

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QY 176 ---GCTGTAGGCGCTTACATTAATATGAAGCTATGCTATGCTCATGTTTGTAT 232

Db 181 TGGCGCTGTAGGCGCTTACATTAATATGAAGCTATGCTATGCTCATGTTTGTAT 240

QY 233 TATGGCTTTACACAGATTACAGAGAGATGATCTGGGATTAACAGCAGCAGAA 292

Db 241 TATGGCTTTACACAGATTACAGAGAGATGATCTGGGATTAACAGCAGCAGAA 300

QY 293 TATAAAGCTTTGATGATGATGAAGATGAAGATGATGATGATGATGATGAT 352

Db 301 TATAAAGCTTTGATGATGATGAAGATGAAGATGATGATGATGATGATGAT 360

QY 353 GGGAGGTTTTCACAGGAGAGCTTATGTTATATATGATGATGATGATGATGAT 412

Db 361 GGGAGGTTTTCACAGGAGAGCTTATGTTATATATGATGATGATGATGATGAT 420

QY 413 ACTGCGAGTGTCACTGACCTAGTTTCTGCTCCACTTCCGAGTTTCTTTCCACAGG 472

Db 421 ACTGCGAGTGTCACTGACCTAGTTTCTGCTCCACTTCCGAGTTTCTTTCCACAGG 480

QY 473 KCCTATCGGTGTCTATAGAGATATTTCTATTTCTCAGTCCACGCGGATTTGACCC 532

Db 481 TCCATCGGTGTCTATAGAGATATTTCTATTTCTCAGTCCACGCGGATTTGACCC 540

QY 533 TTTGGTCCCTGATGTTTGGTCTCTTACGGTGAAGAAACATAAATGTTGATCC 592

Db 541 TTTGGTCCCTGATGTTTGGTCTCTTACGGTGAAGAAACATAAATGTTGATCC 600

QY 593 AGCCATGTGACCTTTAAACCTATGAAGATGATGACAGTTCGTCAACAGGAAAT 652

Db 601 AGCCATGTGACCTTTAAACCTATGAAGATGATGACAGTTCGTCAACAGGAAAT 660

QY 653 GATGATGTCAACCAATTCATTAATCTCCTACCTCCAAATGATGACGTCACTA 709

Db 661 GATGATGTCAACCAATTCATTAATCTCCTACCTCCAAATGATGACGTCACTA 717

RESULT 7
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 LOCUS AGENCOURT_6428540 NIH_MGC_85 Homo sapiens cdna clone IMAGE:5505154
 DEFINITION 5', mRNA sequence.
 ACCESSION BM465006
 VERSION BM465006.1 GI:18514048
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1088)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNL42147 row: k column: 11
High quality sequence stop: 563.

FEATURES	Location/Qualifiers
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BASE COUNT	255 a	300 c	225 g	306 t	2 others
ORIGIN					

Query Match	79.4%;	Score 563;	DB 13;	Length 1088;
Best Local Similarity	89.5%;	Pred. No. 7.1e-157;		
Matches 664;	Conservative 1;	Mismatches 9;	Indels 68;	Gaps 3

Oy	34	CCCGCTCTTCCCTTCGCGTGGCGGTGTGAGCTGAGAGCGGTGTATGTGGGGCAATTAACATGT	93
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Oy	94	CAACCCCGCGTCCGCCCATCTGTGCCCGCGCGCGGGAAGGCACACGCGTGGGTATTTTCC	15
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Db	121	TGCATGGAATTGGAGATATCTGGGGACGAGATGGGCAAGAAAGCTTTGCAAGGTATCAGAAGTT	180
Oy	176	-----GCTGTTAGCCCTGTTACATTAATATATGAACG	207
Db	181	CACATATCAAAATATATCTGCCCGCATGGCGCCTGTTAGGCCCTGTACATTAATATGAACG	240
Oy	208	TGGCTATGCGCTTCATGTTTGATATATTTGGGCGTTTCACAGATTCACAGAGATGAT	267
Db	241	TGGCTATGCGCTTCATGTTTGATATATTTGGGCGTTTCACAGATTCACAGAGATGAT	300
Oy	268	CTGGGATTTAAACAGGACAGAGAAATATAAAGCTTTGATTGATCAGAGCTGAAGAATG	327
Db	301	CTGGGATTTAAACAGGACAGAGAAATATAAAGCTTTGATTGATCAGAGCTGAAGAATG	360
Oy	328	GCATTCCTTTACAGGAATTTATTTGGAGGGTTTCTCAGGGAGAGCTTATCTTAT	387
Db	361	GCATTCCTTTACAGGAATTTATTTGGAGGGTTTCTCAGGGAGAGCTTATCTTAT	420
Oy	388	ATACAGCCCTTACACAGACAGAAACTGGCAGGTGTCACGTGACACTGAGTTCTGCTTC	447
Db	421	ATACAGCCCTTACACAGACAGAAACTGGCAGGTGTCACGTGACACTGAGTTCTGCTTC	480
Oy	448	CACCTTCGGGNTCTTTCACACAGGKCTATTCGGGGTGCTAAAGATATTTCTATTC	507
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Oy	508	TCCAGTGGCACGGGATGTGAACCTTTGGTGTCCCTCATGTTTGGTCTCTTACGGTGG	567
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Oy	568	AAAAACTTAATAATGTTGTAATCCAGCCATGTACCTTTAAACCTATGAAGTATGA	627

Db 601 AAAAATCTANAAACATTTGGTGAATCCAGCAATGTGACCTTTAAAAACCTATGAAGAGTATGA 660

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Qy 688 CTCCAATTGATTGACGTCACCTA 709

Db 720 CTCG - ATTGATTGAGTCTCCCTA 740

RESULT	8
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LOCUS	1300 bp mRNA linear HTC 22-MAY-2001
DEFINITION	Homo sapiens lysophospholipase isoform mRNA, complete cds.
ACCESSION	AF077199
VERSION	AF077199.1 GI:4679011
KEYWORDS	HTC.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens.

REFERENCE AUTHORS	TITLE
1 (bases 1 to 1300)	
Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G., Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W., Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z.	Clooning and functional analysis of cDNAs with open reading frames

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	Genome Res. 10 (10), 1546-1560 (2000) 20493367 11042152 2 (bases 1 to 1300) Shen,Y., Guan,Z., Gu,J., Ye,M., Zhou,J., Zhang,Q., Xu,S., He,K., Chen,S., Mao,M., and Chen,Z. Human Lysophospholipase gene(short form) Unpublished 3 (bases 1 to 1300) Shen,Y.
TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Direct Submission Submitted (10-JUL-1998) Shanghai Institute of Hematology, Shanghai 102 Puti-ting Road IT 102 Puti-ting Road IT

FEATURES

SOURCE

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/db_xref="taxon:9606"
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CDS

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QY 292 ATATTAAGCTTTCATGATCAGAGATGTAATGATGATCTGCTTCAACAGATTAATT 351
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Db 301 TGGAGGGGTTTTCACAGAGAGAGCTTATCTTATATCTGCTTCAACAGAGAGA 360
QY 412 AACTGGCAGGTGTCTACCTCAGTCTGCTTCTGCTTCACTTGGGNTCTTTCACAGG 471
Db 361 AACTGGCAGGTGTCTACCTCAGTCTGCTTCTGCTTCACTTGGGNTCTTTCACAGG 420
QY 472 GKCCATGCGTGTGCTAATAGATATTTCTATCTCCAGTGGCAGGGGATTTGACC 531
Db 421 GTCCATGCGTGTGCTAATAGATATTTCTATCTCCAGTGGCAGGGGATTTGACC 480
QY 532 CTTTGGTCCCTGATGTTGTTGTTCTCTACGTGAGAAAACTAAAAACAATTGGTGAATC 591
Db 481 CTTTGGTCCCTGATGTTGTTGTTCTCTACGTGAGAAAACTAAAAACAATTGGTGAATC 540
QY 592 CAGCAATGTCACCTTTAAACCTATGATGATGATGATGATGATGATGATGATGATGAT 651
Db 541 CAGCAATGTCACCTTTAAACCTATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 652 TGATGATGTCACCAATTCATGATTAACCTCCTACCTCCAAATGATGATGATGATGAT 709
Db 601 TGATGATGTCACCAATTCATGATTAACCTCCTACCTCCAAATGATGATGATGATGAT 658

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RESULT 9
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LOCUS Homo sapiens lysophospholipase mRNA, complete cds.
DEFINITION AF077198.1 GI:4679009
VERSION Homo sapiens.
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1348)
AUTHORS Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G.,
Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W.,
Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.
Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells
JOURNAL Genome Res. 10 (10), 1546-1560 (2000)
MEDLINE 20493367
PUBMED 11042152
REFERENCE 2 (bases 1 to 1348)
AUTHORS Shen,Y., Guan,Z., Gu,J., Ye,M., Zhou,J., Zhang,Q., Xu,S., He,K.,
Chen,S., Mao,M. and Chen,Z.
Human lysophospholipase gene
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1348)
AUTHORS Shen,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1998) Shanghai Institute of Hematology, Shanghai
Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China
FEATURES
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BASE COUNT 392 a 256 c 265 g 435 t
ORIGIN
Query Match 78.9%; Score 559.4; DB 11; Length 1348;
Best local similarity 90.1%; Pred. No. 9, 2e-156;
Matches 636; Conservative 1; Mismatches 3; Indels 66; Gaps 1;
QY 70 GGTGTATGTGCGGCATTAACATGTCACACCCGCTGCGCCGATCGTCCGCGCGGGA 129
Db 1 GGTGTATGTGCGGCATTAACATGTCACACCCGCTGCGCCGATCGTCCGCGCGGGA 60
QY 130 AGGCCACCGCTGCGGATTTTCTGCATGATGATGATGATGATGATGATGATGATGAT 175
Db 61 AGGCCACCGCTGCGGATTTTCTGCATGATGATGATGATGATGATGATGATGATGAT 120
QY 176 -----GCTGTTA 183
Db 121 AAGCCTTTCAGATCAGAGTTCACATATCAATATATCTGCCGATGCGCGCTGTTA 180
QY 184 GGCCTTACATTAATATGAAAGCTATGCTATGCTTATGATTAATGATGATGATGATGAT 243
Db 181 GGCCTTACATTAATATGAAAGCTATGCTATGCTTATGATTAATGATGATGATGATGAT 240
QY 244 CACCAATTCACAGAGAGATGATCTGGATTAACAGCAGCAGAGAGAGAGAGAGAGAGAG 303
Db 241 CACCAATTCACAGAGAGATGATCTGGATTAACAGCAGCAGAGAGAGAGAGAGAGAG 300
QY 304 TGATGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
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Db 541 TGATGTTGGTCTCTTACAGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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Db 601 CCTTAAACCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 664 AGCAATTCATGATTAACCTCCTACCTCCCAATGATGATGATGATGATGATGATGATGAT 709
Db 661 AGCAATTCATGATTAACCTCCTACCTCCCAATGATGATGATGATGATGATGATGATGAT 706
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LOCUS 601462392P1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:386575 5',
DEFINITION mRNA sequence.
ACCESSION BE618034
VERSION BE618034.1 GI:9888972

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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 796)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LLM9609 row: g column: 24
High quality sequence stop: 694.

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:3865775"
/clone_lib="NIH-MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (Phage-resistant)"
/note="Organ: eye; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

BASE COUNT 186 a 196 c 207 g 207 t
ORIGIN
Query Match 78.8%; Score 559; DB 10; Length 796;
Best Local Similarity 88.0%; Pred. No. 1e-155;
Matches 658; Conservative 1; Mismatches 22; Indels 67; Gaps 2;

QY 1 GCGGCTGCAACGCGCTGGGCGCGCGCGCGCGCGCGCTGCGCTGGCGCGCTGCG 60
DB 1 GCGGCTGCAACGCGCTGGGCGCGCGCGCGCGCGCGCTGCGCTGGCGCGCTGCG 60
QY 61 AGCTGAGGCGGTATGTGGCGCAATACATGCAACCCCGCTGCCCGCATGTCGCGG 120
DB 61 AGCTGAGGCGGTATGTGGCGCAATACATGCAACCCCGCTGCCCGCATGTCGCGG 120
QY 121 CCGCGCGGAAGCGCACCGCTGGGCTGATTTCTGCGATGGATTGGAGATCTGG 175
DB 121 CCGCGCGGAAGCGCACCGCTGGGCTGATTTCTGCGATGGATTGGAGATCTGG 180
QY 176 ----- 175
DB 181 GATGGCAGAGCGCTTGCAGATGATGCAATATCAATATATCTGCCCGCATG 240
QY 176 -GCCCTGAGGCGCTTACATTAATATGCAAGCTGCTATGCGCTTCATGATTTAT 234
DB 241 CGGCTGTAGGCGCTTACATTAATATGCAAGCTGCTATGCGCTTCATGATTTAT 300
QY 235 TTGGGCTTACAGATTCACAGAGAGATGATCTGGGATTAAACAGGACGAGAAATA 294
DB 301 TTGGGCTTACAGATTCACAGAGAGATGATCTGGGATTAAACAGGACGAGAAATA 360
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DB 361 TAAAGCTTGTATGATCAAGAGATGAGATGCAATGCTTCTTACAGATTTATTTG 420
QY 355 GAGGCTTTCTCAGAGAGAGCTTTATCTTATATACCTGCGCTTACACAGACAGAAAC 414
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QY 415 TGGCAGGTGTCACACTGACCTAGTTCTGCTTCACTTGGGATTCCTTTCCACAGGAGC 474
DB 415 TGGCAGGTGTCACACTGACCTAGTTCTGCTTCACTTGGGATTCCTTTCCACAGGAGC 474

DB 481 TGGCAGGTGTCACACTGACCTAGTTCTGCGCTTCCACTTGGGCGCTTCTTCCACAGGAGTC 540
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RESULT 11
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DEFINITION 602641734F1 NIH-MGC-61 Homo sapiens cDNA clone IMAGE:4772673 5',
mRNA sequence.
ACCESSION BG614082
VERSION BG614082.1 GI:13665453
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 895)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LLM1643 row: c column: 10
High quality sequence stop: 668.

FEATURES
source
1..895
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4772673"
/clone_lib="NIH-MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDMR-LIB (Clontech); Site_1:
SfiI (ggccgctcgagc); Site_2: SfiI (ggccatattggc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTTATGCCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCGCGCGCGCATG-dT(30)-BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
library."

BASE COUNT 226 a 203 c 215 g 251 t
ORIGIN
Query Match 78.8%; Score 558.4; DB 12; Length 895;
Best Local Similarity 89.6%; Pred. No. 1.6e-155;
Matches 660; Conservative 1; Mismatches 8; Indels 68; Gaps 3;

OY	39	TCTTCCTCCGGTGTGGCGCTAGACGTCAGAGCGSTGTATGTGGCGCAATAAATCAGTCAACC	98
Dd	4	TCTTCCTCCGGTGTGGCGCTGTAGAGCTGAAGCGGTGTATGTGGCGCAATAAATCAGTCAACC	63
OY	99	CCGCTGCCCGGCATGTGTGCCCGCCCGCCCGGAAGGCCACCGCTGCGGGTGATTTCCTCGCAT	158
Dd	64	CCGCTGCCCGGCATGTGTGCCCGCCCGCCCGGAAGGCCACCGCTGCGGGTGATTTCCTCGCAT	123
OY	159	GCATTGGGAGTACTG-----	175
Dd	124	GGAATTGGGAGTACTGGGCGACGATGGGCGAGAAGCCTTGACAGGTATCAGAATTCCAAAT	183
OY	176	-----GCCTGTAGGCGCTGTACAATTAAATATGAACGGCGCT	212
Dd	184	ATCAAATATATGTGCCCGCATCGCGCTGTAGGCGCTGTACAATTAAATATGAACGGCGCT	243
OY	213	ATGCGCTTCAAGTTTGATATTAATTGTGGGCTTTTCACAGATTCACAGAGSAGTGAATGTGG	272
Dd	244	ATGCGCTTCAAGTTTGATATTAATTGTGGGCTTTTCACAGATTCACAGAGSAGTGAATGTGG	303
OY	273	ATTAAACAGGCGACGAGAAAATATAAAGCTTGATTGATCAAGAACTGAAGATGGCATT	332
Dd	304	ATTAAACAGGCGACGAGAAAATATAAAGCTTGATTGATCAAGAACTGAAGATGGCATT	363
OY	333	CCTTCTAACAGATTAATTTGGGAGGGTTTTCTCAGGGGAGGAGCTTATCTTAATAACT	392
Dd	364	CCTTCTAACAGATTAATTTGGGAGGGTTTTCTCAGGGGAGGAGCTTATCTTAATAACT	423
OY	393	GCCCTTACACACAGACAGAAACTGGCAGGTTGCACGTGCACACTAGTTTCTGCTCCACTT	452
Dd	424	GCCCTTACACACAGACAGAAACTGGCAGGTTGCACGTGCACACTAGTTTCTGCTCCACTT	483
OY	453	CGGAGTTCTCTTCCACAGGGKCCATAACGTTGCTGCTAATAGAGATATTTCTATTTCCAG	512
Dd	484	CGGAGTTCTCTTCCACAGGGKCCATAACGTTGCTGCTAATAGAGATATTTCTATTTCCAG	543
OY	513	TGCCAGGGGAGATTGACACCTTGGTTGCCCTCCGATGGTTGGTTCTCTTACGTTGAGAAAA	572
Dd	544	TGCCAGGGGAGATTGACACCTTGGTTGCCCTCCGATGGTTGGTTCTCTTACGTTGAGAAAA	603
OY	573	CTAAAAACATTGGTGAATATCCAGCCAAATGATGACCTTTAAAACTATAGAAGATATGATGAC	632
Dd	604	CTAAAAACATTGGTGAATATCCAGCCCAATGATGACCTTTAAAACTATAGAAGATATGATGAC	663
OY	633	AGTTGTGTCAACAGAGAAATGATGATGTCAAGCAATTCATTGATPA- ACTCCTACCTCC	691
Dd	664	AGTTGTGTCAACAGAG- AATGATGATGTGTGTCAGCAATTCATGATGAAGACTCCTACCTCC	722
OY	692	AATTGATTGAGCTCACT 708	
Dd	723	AATTGATTGAGCTCACT 739	

RESULT	12
B1550895	
LOCUS	
DEFINITION	B1550895 711 bp mRNA linear EST 05-SEP-2001 603195310F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5274938 5' , mRNA sequence.
ACCESSION	B1550895
VERSION	B1550895.1 GI:15438207
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 711) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov
JOURNAL	Tissue Procurement: Miklos Palcovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
COMMENT	

Toshiyuki and Piero Carninci (RIKEN)
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LRAM1694 row: c column: 03
 High quality sequence stop: 708.
 Location/Qualifiers

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/organism="Homo sapiens"
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/clone="IMAGE:5274938"
/clone_1ib="Nih_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site:1: BamHI; Site:2: SalI; xhoI (gtgca
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTYNA-3',
size selected for average insert size 2.5 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carinci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a Nih_MGC library."

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Query Match	78.68;	Score 557.6;	DB 13;	Length 711;
Best Local Similarity	89.7%;	Pred. No. 2.5e-155;		
Matches 636; Conservative	1;	Mismatches 6;	Indels 66;	Gaps 1

QY	47	CCGTTGCGGTGAGCTGACGAGCGGGTATGTGCGCGCAATTAACATATGCAACCCCGCGTCC	106
Db	3	CGGGCTGCGCTGTGAGACTGAGCGGCTGTATGTGCGCATATGTCAACCCCGCTGCC	62
QY	107	CGCATTCGTGCCCGCCGCCGGAAGGCCACCGCTCGGCTGATTTTTCCTGCATGGATGGG	166
Db	63	CGCATTCGTGCCCGCCGCCGGAAGGCCACCGCTCGGCTGATTTTTCCTGCATGGATGGG	122
QY	167	AGATCTGG-----	175
Db	123	AGATCTGGGCGACGATGGGCGAAGACCTTTGCAGTATCAGAACTTCACATATCAATTA	182
QY	176	-----GCTGTTAGGCTGTATACATTAATATGAAGCGGTATGCTTC	220
Db	183	TATCTCGCCGCGCATGGCGCTGTAGGCTGTATCAATTAATATGAACGTGGCTATGCTTC	242
QY	221	ATGCTTTGATATTATTATTTGGCTTTCACCGATTCACAGAGAGATCAATCTGGATTTAAAC	280
Db	243	ATGCTTTGATATTATTATTTGGCTTTCACCGATTCACAGAGAGATCAATCTGGATTTAAAC	302
QY	281	GGAGCAGAAAATATATAAGCTTTTATTTGATCAAGAAAGTGAAGATGGCATCTCTCTAA	340
Db	303	GGAGCAGAAAATATATAAGCTTTTATTTGATCAAGAAAGTGAAGATGGCATCTCTCTAA	362
QY	341	CACAATTTATTTTGGAGGGGTTTTCACAGAGAGAGACTTATCTTATATACGCGCTTAC	400
Db	363	CACAATTTATTTTGGAGGGGTTTTCACAGAGAGAGACTTATCTTATATACGCGCTTAC	422
QY	401	CACACAGCAGAAACTGGCAGGTGTCACTGCACCTCAGTTCTTGCTTCCACTTCGGAGATTC	460
Db	423	CACACAGCAGAAACTGGCAGGTGTCACTGCACCTCAGTTCTTGCTTCCACTTCGGAGATTC	482
QY	461	CTTTCCACAGGGKCCATTCGCTGTGGTGTGCTAATATGAGATATTTCTATTTCTCCAGTGCACAG	520
Db	483	CTTTCCACAGGGKCCATTCGCTGTGGTGTGCTAATATGAGATATTTCTATTTCTCCAGTGCACAG	542
QY	521	GGATTTGACACTTTGGTGTCCCTCATTTGGTTCCTTACGGTGGAAAACTTAAAAAC	580
Db	543	GGATTTGACACTTTGGTGTCCCTCATTTGGTTCCTTACGGTGGAAAACTTAAAAAC	602
QY	581	ATTGGTGAATTCAGCCAAATGTGACCTTTAAACCTATGAAGGTATGATGCACAGTTCTGTG	640

contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

BASE COUNT 178 a 157 c 173 g 201 t

ORIGIN

Query Match 76.3%; Score 540.8; DB 12; Length 709;
Best Local Similarity 89.1%; Pred. No. 2.6e-150;
Matches 632; Conservative 1; Mismatches 9; Indels 67; Gaps 2;

49 GCTTCGCTGTAGCTGAGGGGTATGTGCGCAATTAATGCAACCCCGTCCCG 108
1 GCTTCGCTGTAGCTGAGGGGTATGTGCGCAATTAATGCAACCCCGTCCCG 60
109 CCATGTCGCGCCGCCGCGGAGGACCCGCTGCGGTATTTCTCGATGATGGAG 168
61 CCATGTCGCGCCGCCGCGGAGGACCCGCTGCGGTATTTCTCGATGATGGAG 120
169 ATACTGG----- 175
121 ATACTGGCAGGATGGCAGAGCCTTGCAGGATCAGAAATTCATATCAATATA 180
176 -----GCTTTAGCCTGTTACATTAAATATGACGCGGCTATGCTTCAT 222
181 TCTGCCCGCATGCGCTGTAGCCTGTTACATTAAATATGACGCTGCTATGCTTCAT 240
223 GATTGATATTATGGGCTTACCAGATTCACAGAGGATGATGCGGATTAACAGG 282
241 GATTGATATTATGGGCTTACCAGATTCACAGAGGATGATGCGGATTAACAGG 300
283 CAGCAGAAATATATAAGCTTTGATTCAGAGAGTGAAGATGCGATTCCTCTAACA 342
301 CAGCAGAAATATATAAGCTTTGATTCAGAGAGTGAAGATGCGATTCCTCTAACA 360
343 GAATATTATTTGGAGGCTTTCTCAGGAGAGCTTTATCTTATPACTGCCCTTACCA 402
361 GAATATTATTTGGAGGCTTTCTCAGGAGAGCTTTATCTTATPACTGCCCTTACCA 420
403 CACAGCAAACTGGCAGGTGTCACGTGCTTCTGCTTCCGCTCCGCTGCTTCCCT 462
421 CACAGCAAACTGGCAGGTGTCACGTGCTTCTGCTTCCGCTCCGCTGCTTCCCT 480
463 TTCCACAGAGGCTATGCGGTGCTCTAATAGATATTCTTCTCAGTGCACAGGG 522
481 TTCCACAGAGGCTATGCGGTGCTCTAATAGATATTCTTCTCAGTGCACAGGG 540
523 ATGTGACCCCTTTGGTCCCTGATGTTGTTGTTCTTACGCTGGAATAAACAAT 582
541 ATGTGACCCCTTTGGTCCCTGATGTTGTTGTTCTTACGCTGGAATAAACAAT 600
583 TGTGTAATCCAGCAATGTGACCTTTAAACCTATGAAGGATGACAGAGTCCGCTG 642
601 TGTGTAATCCAGCAATGTGACCTTTAAACCTATGAAGGATGACAGAGTCCGCTG 660
643 AACAGGAATGATGATGCTCAAGCA-TTCATTGATTAACCTCTACTCC 690
661 AACAGGAATGATGATGCTCAAGCAATTCATTGATTAACCTACTTC 709

RESULT 15
LOCUS B1596291 725 bp mRNA linear EST 07-SEP-2001
DEFINITION 603243007F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285569 5', mRNA sequence.
ACCESSION B1596291
VERSION B1596291.1 GI:15488702
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 725)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1721 row: n column: 02
High quality sequence stop: 721.

FEATURES
source
location/Qualifiers
1..725
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/note="Organ: brain; Vector: pBluescript (modified pluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to R07 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 165 a 177 c 194 g 188 t 1 others

Query Match 75.4%; Score 534.6; DB 13; Length 725;
Best Local Similarity 89.3%; Pred. No. 1.9e-148;
Matches 624; Conservative 1; Mismatches 7; Indels 67; Gaps 2;

1 GCCGCTGCACGCCCTTTGGGCGCGCGCGCGCTTCTTCCGCTGCGCTG 60
27 GCCGCTGCACGCCCTTTGGGCGCGCGCGCGCTTCTTCCGCTGCGCTG 86
61 AGCTGAGCGGTATGTGCGGCAATACATGCAACCCCGCGCCGATGTCGCGG 120
87 AGCTGAGCGGTATGTGCGGCAATACATGCAACCCCGCGCGCGATGTCGCGG 146
121 CCGCCGGAAGGCCACCGCTGCGGTATTTCTGTCATGATGGAGATAGCTGG 175
147 CCGCCGGAAGGCCACCGCTGCGGTATTTCTGTCATGATGGAGATAGCTGG 206
176 ----- 175
207 GATGGCAGAAAGCCTTTGAGGATGATGAGAGTTCAATATATATGCCCCGATG 266
176 -GCCCTTAGGCGCTGTACATTAAATATGACGCTGATGCTTCATGATTTA 234
267 CGCCTTTAGCGCTGTACATTAAATATGACGCTGATGCTTCATGATTTA 326
235 TTGGGCTTTCACAGATTCACAGAGGATGAATCTGGATTAACAGCAGCAATA 294
327 TTGGGCTTTCACAGATTCACAGAGGATGAATCTGGATTAACAGCAGCAATA 386
295 TAAAGCTTTGATGATGCAAGAAAGTGAATGCAATCTCTCTCAAGATATTTGG 354
387 TAAAGCTTTGATGATGCAAGAAAGTGAATGCAATCTCTCTCAAGATATTTGG 446
355 GAGGCTTTCTCAGAGAGAGCTTTATCTTATATCTCCCTTACACAGCAGCAAC 414
447 GAGGCTTTCTCAGAGAGAGCTTTATCTTATATCTCCCTTACACAGCAGCAAC 506
415 TGGCAGGTTCACGTGACGCTTCTTCTTCCACTTCCGAGTTCCTTCCACAGGKC 474

Db 507 TGGCAGGTGCTACCTGCACTGCTGCTTCCACTTCGGGCTTCCTTCCACAGGCTC 566
Qy 475 CTATCGGTGGTGCCTAATAGAGATATTCTATTCCTCAGTGCACGGGATTTGACCTT 534
|||||
Db 567 CTATCGGTGGTGCCTAATAGAGATATTCTATTCCTCAGTGCACGGGATTTGACCTT 626
535 TGGTCCCCCTGATGTTGGTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAG 594
|||||
Db 627 TGGTCCCCCTGATG-TGGTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAA 685
Qy 595 CCATGTGACCTTTAAACCTATGAGGTATGATGCACA 633
|||||
Db 686 GCATGTGACCTTTAAACCTATGAGGTATGATGCACA 724

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